

SEQUENCE LISTING

<110> Yocum, R. et al.

<120> METHODS AND MICROORGANISMS FOR PRODUCTION OF
PANTO-COMPOUNDS

<130> BGI-141CP

<140>

<141>

<150> USSN 09/400,494

<151> 1999-09-21

<150> USSN 60/210,072

<151> 2000-06-07

<150> USSN 60/221,836

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<150> USSN 60/221,836

<151> 2000-08-24

<160> 94

<170> PatentIn Ver. 2.0

<210> 1

<211> 311

<212> PRT

<213> Haemophilus influenzae

<400> 1

Met	Glu	Phe	Ser	Thr	Gln	Gln	Thr	Pro	Phe	Leu	Ser	Phe	Asn	Arg	Glu
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Gln	Trp	Ala	Glu	Leu	Arg	Lys	Ser	Val	Pro	Leu	Lys	Leu	Thr	Glu	Gln
			20					25					30		

Asp	Leu	Lys	Pro	Leu	Leu	Gly	Phe	Asn	Glu	Asp	Leu	Ser	Leu	Asp	Glu
		35					40					45			

Val	Ser	Thr	Ile	Tyr	Leu	Pro	Leu	Thr	Arg	Leu	Ile	Asn	Tyr	Tyr	Ile
	50					55					60				

Asp	Glu	Asn	Leu	His	Arg	Gln	Thr	Val	Leu	His	Arg	Phe	Leu	Gly	Arg
	65				70					75					80

Asn	Asn	Ala	Lys	Thr	Pro	Tyr	Ile	Ile	Ser	Ile	Ala	Gly	Ser	Val	Ala
			85						90					95	

Val	Gly	Lys	Ser	Thr	Ser	Ala	Arg	Ile	Leu	Gln	Ser	Leu	Leu	Ser	His
		100						105					110		

Trp	Pro	Thr	Glu	Arg	Lys	Val	Asp	Leu	Ile	Thr	Thr	Asp	Gly	Phe	Leu
		115					120					125			

Tyr	Pro	Leu	Asn	Lys	Leu	Lys	Gln	Asp	Asn	Leu	Leu	Gln	Lys	Lys	Gly
		130				135						140			

Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
 145 150 155 160
 Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
 165 170 175
 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
 180 185 190
 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
 195 200 205
 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
 210 215 220
 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
 225 230 235 240
 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
 245 250 255
 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
 260 265 270
 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
 275 280 285
 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
 290 295 300
 Glu Leu Ile Lys Leu Arg Lys
 305 310

<210> 2
 <211> 316
 <212> PRT
 <213> Escherichia coli

<400> 2
 Met Ser Ile Lys Glu Gln Thr Leu Met Thr Pro Tyr Leu Gln Phe Asp
 1 5 10 15
 Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser
 20 25 30
 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
 35 40 45
 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
 50 55 60
 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu Glu Gln Phe Leu
 65 70 75 80
 Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
 85 90 95
 Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
 100 105 110

Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
 115 120 125
 Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
 130 135 140
 Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
 145 150 155 160
 Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
 165 170 175
 His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
 180 185 190
 Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
 195 200 205
 Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
 210 215 220
 Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
 225 230 235 240
 Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
 245 250 255
 Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
 260 265 270
 Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
 275 280 285
 Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
 290 295 300
 Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
 305 310 315

<110> 3

<111> 319

<112> PRT

<113> Bacillus subtilis

<400> 3

Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
 1 5 10 15
 Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
 20 25 30
 Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
 35 40 45
 Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
 50 55 60
 His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
 65 70 75 80

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<210> 4
<211> 312
<212> PRT
<213> Mycobacterium leprae
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Met  Pro  Arg  Leu  Ser  Glu  Pro  Ser  Pro  Tyr  Val  Glu  Phe  Asp  Arg  Lys
  1              5              10              15

Gln  Trp  Arg  Ala  Leu  Arg  Met  Ser  Thr  Pro  Leu  Ala  Leu  Thr  Glu  Glu
          20              25              30

Glu  Leu  Ile  Gly  Leu  Arg  Gly  Leu  Gly  Glu  Gln  Ile  Asp  Leu  Leu  Glu
          35              40              45
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Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
 50 55 60
 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
 55 70 75 80
 Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala
 35 90 95
 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
 100 105 110
 Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr
 115 120 125
 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met
 130 135 140
 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
 145 150 155 160
 Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val
 165 170 175
 Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val
 180 185 190
 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
 195 200 205
 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
 210 215 220
 Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
 225 230 235 240
 Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
 245 250 255
 Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile
 260 265 270
 Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
 275 280 285
 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
 290 295 300
 Asn Arg Leu Arg Leu Arg Lys Leu
 305 310

<210> 5

<211> 312

<212> PRT

<213> Mycobacterium tuberculosis

<400> 5

Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg
 1 5 10 15

Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
20 25 30

Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
35 40 45

Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
50 55 60

Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
65 70 75 80

Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala
85 90 95

Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
100 105 110

Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr
115 120 125

Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met
130 135 140

His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
145 150 155 160

Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val
165 170 175

Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val
180 185 190

Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
195 200 205

Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
210 215 220

Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
225 230 235 240

Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
245 250 255

Tyr Ala Ala Phe Ser Asp Ser Gln Ala Val Val Ala Ala Arg Glu Ile
260 265 270

Trp Arg Thr Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
275 280 285

Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
290 295 300

Asn Arg Leu Arg Leu Arg Lys Leu
305 310

<210> 6

<211> 329

<212> PRT

<213> Streptomyces coelicolor

<400> 6

Met	Ile	Ser	Pro	Val	Pro	Ser	Ile	Pro	Arg	Ser	Ala	His	Arg	Gln	Arg
1				5					10					15	
Pro	Glu	Ala	Thr	Pro	Tyr	Val	Asp	Leu	Thr	Arg	Pro	Glu	Trp	Ser	Ala
			20					25					30		
Leu	Arg	Asp	Lys	Thr	Pro	Leu	Pro	Leu	Thr	Ala	Glu	Glu	Val	Glu	Lys
		35					40					45			
Leu	Arg	Gly	Leu	Gly	Asp	Val	Ile	Asp	Leu	Asp	Glu	Val	Arg	Asp	Ile
	50					55					60				
Tyr	Leu	Pro	Leu	Ser	Arg	Leu	Leu	Asn	Leu	Tyr	Val	Gly	Ala	Thr	Asp
65					70					75					80
Gly	Leu	Arg	Gly	Ala	Leu	Asn	Thr	Phe	Leu	Gly	Glu	Gln	Gly	Ser	Gln
				85					90					95	
Ser	Gly	Thr	Pro	Phe	Val	Ile	Gly	Val	Ala	Gly	Ser	Val	Ala	Val	Gly
			100					105					110		
Lys	Ser	Thr	Val	Ala	Arg	Leu	Leu	Gln	Ala	Leu	Leu	Ser	Arg	Trp	Pro
		115					120					125			
Glu	His	Pro	Arg	Val	Glu	Leu	Val	Thr	Thr	Asp	Gly	Phe	Leu	Leu	Pro
	130					135					140				
Thr	Arg	Glu	Leu	Glu	Ala	Arg	Gly	Leu	Met	Ser	Arg	Lys	Gly	Phe	Pro
145					150					155					160
Glu	Ser	Tyr	Asp	Arg	Arg	Ala	Leu	Thr	Arg	Phe	Val	Ala	Asp	Ile	Lys
				165					170					175	
Ala	Gly	Lys	Ala	Glu	Val	Thr	Ala	Pro	Val	Tyr	Ser	His	Leu	Ile	Tyr
			180					185					190		
Asp	Ile	Val	Pro	Asp	Gln	Arg	Leu	Val	Val	Arg	Arg	Pro	Asp	Ile	Leu
		195					200					205			
Ile	Val	Glu	Gly	Leu	Asn	Val	Leu	Gln	Pro	Ala	Leu	Pro	Gly	Lys	Asp
	210					215					220				
Gly	Arg	Thr	Arg	Val	Gly	Leu	Ala	Asp	Tyr	Phe	Asp	Phe	Ser	Val	Tyr
225					230					235					240
Val	Asp	Ala	Arg	Thr	Glu	Asp	Ile	Glu	Arg	Trp	Tyr	Leu	Asn	Arg	Phe
				245					250					255	
Arg	Lys	Leu	Arg	Ala	Thr	Ala	Phe	Gln	Asn	Pro	Ser	Ser	Tyr	Phe	Arg
			260					265					270		
Lys	Tyr	Thr	Gln	Val	Ser	Glu	Glu	Glu	Ala	Leu	Asp	Tyr	Ala	Arg	Thr
		275					280					285			
Thr	Trp	Arg	Thr	Ile	Asn	Lys	Pro	Asn	Leu	Val	Glu	Asn	Val	Ala	Pro
	290					295					300				
Thr	Arg	Gly	Arg	Ala	Thr	Leu	Val	Leu	Arg	Lys	Gly	Pro	Asp	His	Lys

Val Gln Arg Leu Ser Leu Arg Lys Leu
325

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<210> 7
<211> 265
<212> PRT
<213> Streptomyces coelicolor
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<400> 7
Met Leu Leu Thr Ile Asp Val Gly Asn Thr His Thr Val Leu Gly Leu
  1                   5                10               15
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Phe Asp Gly Glu Asp Ile Val Glu His Trp Arg Ile Ser Thr Asp Ser
20 25 30

Arg Arg Thr Ala Asp Glu Leu Ala Val Leu Leu Gln Gly Leu Met Gly
35 40 45

Met His Pro Leu Leu Gly Asp Glu Leu Gly Asp Gly Ile Asp Gly Ile
50 55 60

Ala Ile Cys Ala Thr Val Pro Ser Val Leu His Glu Leu Arg Glu Val
55 70 75 80

Thr Arg Arg Tyr Tyr Gly Asp Val Pro Ala Val Leu Val Glu Pro Gly
85 90 95

Val Lys Thr Gly Val Pro Ile Leu Thr Asp His Pro Lys Glu Val Gly
100 105 110

Ala Asp Arg Ile Ile Asn Ala Val Ala Ala Val Glu Leu Tyr Gly Gly
115 120 125

Pro Ala Ile Val Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Ala Val
130 135 140

Ser Ala Arg Gly Glu Tyr Ile Gly Gly Val Ile Ala Pro Gly Ile Glu
145 150 155 160

Ile Ser Val Glu Ala Leu Gly Val Lys Gly Ala Gln Leu Arg Lys Ile
165 170 175

Glu Val Ala Arg Pro Arg Ser Val Ile Gly Lys Asn Thr Val Glu Ala
180 185 190

Met Gln Ser Gly Ile Val Tyr Gly Phe Ala Gly Gln Val Asp Gly Val
195 200 205

Val Asn Arg Met Ala Arg Glu Leu Ala Asp Asp Pro Asp Asp Val Thr
210 215 220

Val Ile Ala Thr Gly Gly Leu Ala Pro Met Val Leu Gly Glu Ser Ser
225 230 235 240

Val Ile Asp Glu His Glu Pro Trp Leu Thr Leu Met Gly Leu Arg Leu
245 250 255

Val Tyr Glu Arg Asn Val Ser Arg Met

260

265

<210> 8

<211> 272

<212> PRT

<213> Mycobacterium tuberculosis

<400> 8

Met	Leu	Leu	Ala	Ile	Asp	Val	Arg	Asn	Thr	His	Thr	Val	Val	Gly	Leu
1				5					10					15	

Leu	Ser	Gly	Met	Lys	Glu	His	Ala	Lys	Val	Val	Gln	Gln	Trp	Arg	Ile
			20					25						30	

Arg	Thr	Glu	Ser	Glu	Val	Thr	Ala	Asp	Glu	Leu	Ala	Leu	Thr	Ile	Asp
		35					40					45			

Gly	Leu	Ile	Gly	Glu	Asp	Ser	Glu	Arg	Leu	Thr	Gly	Thr	Ala	Ala	Leu
	50					55					60				

Ser	Thr	Val	Pro	Ser	Val	Leu	His	Glu	Val	Arg	Ile	Met	Leu	Asp	Gln
	65				70					75					80

Tyr	Trp	Pro	Ser	Val	Pro	His	Val	Leu	Ile	Glu	Pro	Gly	Val	Arg	Thr
				85					90					95	

Gly	Ile	Pro	Leu	Leu	Val	Asp	Asn	Pro	Lys	Glu	Val	Gly	Ala	Asp	Arg
			100					105					110		

Ile	Val	Asn	Cys	Leu	Ala	Ala	Tyr	Asp	Arg	Phe	Arg	Lys	Ala	Ala	Ile
		115					120					125			

Val	Val	Asp	Phe	Gly	Ser	Ser	Ile	Cys	Val	Asp	Val	Val	Ser	Ala	Lys
	130					135					140				

Gly	Glu	Phe	Leu	Gly	Gly	Ala	Ile	Ala	Pro	Gly	Val	Gln	Val	Ser	Ser
145					150					155					160

Asp	Ala	Ala	Ala	Ala	Arg	Ser	Ala	Ala	Leu	Arg	Arg	Val	Glu	Leu	Ala
				165					170					175	

Arg	Pro	Arg	Ser	Val	Val	Gly	Lys	Asn	Thr	Val	Glu	Cys	Met	Gln	Ala
			180					185					190		

Gly	Ala	Val	Phe	Gly	Phe	Ala	Gly	Leu	Val	Asp	Gly	Leu	Val	Gly	Arg
		195					200					205			

Ile	Arg	Glu	Asp	Val	Ser	Gly	Phe	Ser	Val	Asp	His	Asp	Val	Ala	Ile
	210					215					220				

Val	Ala	Thr	Gly	His	Thr	Ala	Pro	Leu	Leu	Leu	Pro	Glu	Leu	His	Thr
225					230					235					240

Val	Asp	His	Tyr	Asp	Gln	His	Leu	Thr	Leu	Gln	Gly	Leu	Arg	Leu	Val
				245					250					255	

Phe	Glu	Arg	Asn	Leu	Glu	Val	Gln	Arg	Gly	Arg	Leu	Lys	Thr	Ala	Arg
			260					265						270	

[illegible]

<210> 10
 <211> 262
 <212> PET
 <213> *Deinococcus radiopugnans*

<400> 10

Met	Pro	Ala	Phe	Pro	Leu	Leu	Ala	Val	Asp	Ile	Gly	Asn	Thr	Thr	Thr
1				5					10					15	
Val	Leu	Gly	Leu	Ala	Asp	Ala	Ser	Gly	Ala	Leu	Thr	His	Thr	Trp	Arg
			20					25					30		
Ile	Arg	Thr	Asn	Arg	Glu	Met	Leu	Pro	Asp	Asp	Leu	Ala	Leu	Gln	Leu
		35					40					45			
His	Gly	Leu	Phe	Thr	Leu	Ala	Gly	Ala	Pro	Ile	Pro	Arg	Ala	Ala	Val
	50					55					60				
Leu	Ser	Ser	Val	Ala	Pro	Pro	Val	Gly	Glu	Asn	Tyr	Ala	Leu	Ala	Leu
65					70					75					80
Lys	Arg	His	Phe	Met	Ile	Asp	Ala	Phe	Ala	Val	Ser	Ala	Glu	Asn	Leu
				85					90					95	
Pro	Asp	Val	Thr	Val	Glu	Leu	Asp	Thr	Pro	Gly	Ser	Val	Gly	Ala	Asp
			100					105					110		
Arg	Leu	Cys	Asn	Leu	Phe	Gly	Ala	Glu	Lys	Tyr	Leu	Gly	Gly	Leu	Asp
		115					120					125			
Tyr	Ala	Val	Val	Val	Asp	Phe	Gly	Thr	Ser	Thr	Asn	Phe	Asp	Val	Val
	130					135					140				
Gly	Arg	Gly	Arg	Arg	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Thr	Gly	Ala	Gln
145					150					155					160
Val	Ser	Ala	Asp	Ala	Leu	Phe	Ala	Arg	Ala	Ala	Lys	Leu	Pro	Arg	Ile
				165					170					175	
Thr	Leu	Gln	Ala	Pro	Glu	Thr	Ala	Ile	Gly	Lys	Asn	Thr	Val	His	Ala
			180					185					190		
Leu	Gln	Ser	Gly	Leu	Val	Phe	Gly	Tyr	Ala	Glu	Met	Val	Asp	Gly	Leu
		195					200					205			
Leu	Arg	Arg	Ile	Arg	Ala	Glu	Leu	Pro	Gly	Glu	Ala	Val	Ala	Val	Ala
	210					215					220				
Thr	Gly	Gly	Phe	Ser	Arg	Thr	Val	Gln	Gly	Ile	Cys	Gln	Glu	Ile	Asp
225					230					235					240
Tyr	Tyr	Asp	Glu	Thr	Leu	Thr	Leu	Arg	Gly	Leu	Val	Glu	Leu	Trp	Ala
				245					250					255	
Ser	Arg	Ser	Glu	Val	Arg										
				260											

<210> 11
 <211> 212
 <212> PRT

<213> Desulfovibrio vulgaris

<400> 11

Met Thr Gln His Phe Leu Leu Phe Asp Ile Gly Asn Thr Asn Val Lys
 1 5 10 15

Ile Gly Ile Ala Val Glu Thr Ala Val Leu Thr Ser Tyr Val Leu Pro
 20 25 30

Thr Asp Pro Gly Gln Thr Thr Asp Ser Ile Gly Leu Arg Leu Leu Glu
 35 40 45

Val Leu Arg His Ala Gly Leu Gly Pro Ala Asp Val Gly Ala Cys Val
 50 55 60

Ala Ser Ser Val Val Pro Gly Val Asn Pro Leu Ile Arg Arg Ala Cys
 65 70 75 80

Glu Arg Tyr Leu Tyr Arg Lys Leu Leu Phe Ala Pro Gly Asp Ile Ala
 85 90 95

Ile Pro Leu Asp Asn Arg Tyr Glu Arg Pro Ala Glu Val Gly Ala Asp
 100 105 110

Arg Leu Val Ala Ala Tyr Ala Ala Arg Arg Leu Tyr Pro Gly Pro Arg
 115 120 125

Ser Leu Val Ser Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Cys Val
 130 135 140

Glu Gly Gly Ala Tyr Leu Gly Gly Leu Ile Cys Pro Gly Val Leu Ser
 145 150 155 160

Ser Ala Gly Ala Leu Ser Ser Arg Thr Ala Lys Leu Pro Arg Ile Ser
 165 170 175

Leu Glu Val Glu Glu Asp Ser Pro Val Ile Gly Arg Ser Thr Thr Thr
 180 185 190

Ser Leu Asn His Gly Phe Ile Phe Gly Phe Ala Ala Met Thr Glu Gly
 195 200 205

Val Leu Ala Ala
 210

<210> 12

<211> 246

<212> PRT

<213> Thermotoga maritima

<400> 12

Met Tyr Leu Leu Val Asp Val Gly Asn Thr His Ser Val Phe Ser Ile
 1 5 10 15

Thr Glu Asp Gly Lys Thr Phe Arg Arg Trp Arg Leu Ser Thr Gly Val
 20 25 30

Phe Gln Thr Glu Asp Glu Leu Phe Ser His Leu His Pro Leu Leu Gly
 35 40 45

Asp Ala Met Arg Glu Ile Lys Gly Ile Gly Val Ala Ser Val Val Pro
 50 55 60
 Thr Gln Asn Thr Val Ile Glu Arg Phe Ser Gln Lys Tyr Phe His Ile
 65 70 75 80
 Ser Pro Ile Trp Val Lys Ala Lys Asn Gly Cys Val Lys Trp Asn Val
 85 90 95
 Lys Asn Pro Ser Glu Val Gly Ala Asp Arg Val Ala Asn Val Val Ala
 100 105 110
 Phe Val Lys Glu Tyr Gly Lys Asn Gly Ile Ile Ile Asp Met Gly Thr
 115 120 125
 Ala Thr Thr Val Asp Leu Val Val Asn Gly Ser Tyr Glu Gly Gly Ala
 130 135 140
 Ile Leu Pro Gly Phe Phe Met Met Val His Ser Leu Phe Arg Gly Thr
 145 150 155 160
 Ala Lys Leu Pro Leu Val Glu Val Lys Pro Ala Asp Phe Val Val Gly
 165 170 175
 Lys Asp Thr Glu Glu Asn Ile Arg Leu Gly Val Val Asn Gly Ser Val
 180 185 190
 Tyr Ala Leu Glu Gly Ile Ile Gly Arg Ile Lys Glu Val Tyr Gly Asp
 195 200 205
 Leu Pro Val Val Leu Thr Gly Gly Gln Ser Lys Ile Val Lys Asp Met
 210 215 220
 Ile Lys His Glu Ile Phe Asp Glu Asp Leu Thr Ile Lys Gly Val Tyr
 225 230 235 240
 His Phe Cys Phe Gly Asp
 245

<210> 13

<211> 273

<212> PRT

<213> Treponema pallidum

<400> 13

Met Leu Leu Ile Asp Val Gly Asn Ser His Val Val Phe Gly Ile Gln
 1 5 10 15
 Gly Glu Asn Gly Gly Arg Val Cys Val Arg Glu Leu Phe Arg Leu Ala
 20 25 30
 Pro Asp Ala Arg Lys Thr Gln Asp Glu Tyr Ser Leu Leu Ile His Ala
 35 40 45
 Leu Cys Glu Arg Ala Gly Val Gly Arg Ala Ser Leu Arg Asp Ala Phe
 50 55 60
 Ile Ser Ser Val Val Pro Val Leu Thr Lys Thr Ile Ala Asp Ala Val
 65 70 75 80

Asn

<400> 14

Met 1	Asn	Lys	Pro	Leu 5	Leu	Ser	Glu	Leu	Ile 10	Ile	Asp	Ile	Gly	Asn 15	Thr
Ser	Ile	Ala	Phe 20	Ala	Leu	Phe	Lys	Asp 25	Asn	Gln	Val	Asn	Leu 30	Phe	Ile
Lys	Met	Lys 35	Thr	Asn	Leu	Met	Leu 40	Arg	Tyr	Asp	Glu	Val 45	Tyr	Ser	Phe
Phe 50	Glu	Glu	Asn	Phe	Asp	Phe 55	Asn	Val	Asn	Lys	Val 60	Phe	Ile	Ser	Ser
Val 65	Val	Pro	Ile	Leu	Asn 70	Glu	Thr	Phe	Lys	Asn 75	Val	Ile	Phe	Ser	Phe 80

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<210> 15
<211> 229
<212> PRT
<213> Aquifex aeolicus
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<400> 15
Met  Arg  Phe  Leu  Thr  Val  Asp  Val  Gly  Asn  Ser  Ser  Val  Asp  Ile  Ala
   1                                10                      15

Leu  Trp  Glu  Gly  Lys  Lys  Val  Lys  Asp  Phe  Leu  Lys  Leu  Ser  His  Glu
                20                      25                      30

Glu  Phe  Leu  Lys  Glu  Glu  Phe  Pro  Lys  Leu  Lys  Ala  Leu  Gly  Ile  Ser
                35                      40                      45

Val  Lys  Gln  Ser  Phe  Ser  Glu  Lys  Val  Arg  Gly  Lys  Ile  Pro  Lys  Ile
   50                                55                      60

Lys  Phe  Leu  Lys  Lys  Glu  Asn  Phe  Pro  Ile  Gln  Val  Asp  Tyr  Lys  Thr
   65                                70                      75                      80

Pro  Glu  Thr  Leu  Gly  Thr  Asp  Arg  Val  Ala  Leu  Ala  Tyr  Ser  Ala  Lys
                85                      90                      95

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Lys Phe Tyr Gly Lys Asn Val Val Val Ile Ser Ala Gly Thr Ala Leu
 100 105 110
 Val Ile Asp Leu Val Leu Glu Gly Lys Phe Lys Gly Gly Phe Ile Thr
 115 120 125
 Leu Gly Leu Gly Lys Lys Leu Lys Ile Leu Ser Asp Leu Ala Glu Gly
 130 135 140
 Ile Pro Glu Phe Phe Pro Glu Glu Val Glu Ile Phe Leu Gly Arg Ser
 145 150 155 160
 Thr Arg Glu Cys Val Leu Gly Gly Ala Tyr Arg Glu Ser Thr Glu Phe
 165 170 175
 Ile Lys Ser Thr Leu Lys Leu Trp Arg Lys Val Phe Lys Arg Lys Phe
 180 185 190
 Lys Val Val Ile Thr Gly Gly Glu Gly Lys Tyr Phe Ser Lys Phe Gly
 195 200 205
 Ile Tyr Asp Pro Leu Leu Val His Arg Gly Met Arg Asn Leu Leu Tyr
 210 215 220
 Leu Tyr His Arg Ile
 225

<210> 16
 <211> 257
 <212> PRT
 <213> Synechocystis sp.

<400> 16
 Met Glu Thr Ser Lys Pro Gly Cys Gly Leu Ala Leu Asp Asn Asp Lys
 1 5 10 15
 Gln Lys Pro Trp Leu Gly Leu Met Ile Gly Asn Ser Arg Leu His Trp
 20 25 30
 Ala Tyr Cys Ser Gly Asn Ala Pro Leu Gln Thr Trp Val Thr Asp Tyr
 35 40 45
 Asn Pro Lys Ser Ala Gln Leu Pro Val Leu Leu Gly Lys Val Pro Leu
 50 55 60
 Met Leu Ala Ser Val Val Pro Glu Gln Thr Glu Val Trp Arg Val Tyr
 65 70 75 80
 Gln Pro Lys Ile Leu Thr Leu Lys Asn Leu Pro Leu Val Asn Leu Tyr
 85 90 95
 Pro Ser Phe Gly Ile Asp Arg Ala Leu Ala Gly Leu Gly Thr Gly Leu
 100 105 110
 Thr Tyr Gly Phe Pro Cys Leu Val Val Asp Gly Gly Thr Ala Leu Thr
 115 120 125
 Ile Thr Gly Phe Asp Gln Asp Lys Lys Leu Val Gly Gly Ala Ile Leu
 130 135 140

Pro Gly Leu Gly Leu Gln Leu Ala Thr Leu Gly Asp Arg Leu Ala Ala
 145 150 155 160
 Leu Pro Lys Leu Glu Met Asp Gln Leu Thr Glu Leu Pro Asp Arg Trp
 165 170 175
 Ala Leu Asp Thr Pro Ser Ala Ile Phe Ser Gly Val Val Tyr Gly Val
 180 185 190
 Leu Gly Ala Leu Gln Ser Tyr Leu Gln Asp Trp Gln Lys Leu Phe Pro
 195 200 205
 Gly Ala Ala Met Val Ile Thr Gly Gly Asp Gly Lys Ile Leu His Gly
 210 215 220
 Phe Leu Lys Glu His Ser Pro Asn Leu Ser Val Ala Trp Asp Asp Asn
 225 230 235 240
 Leu Ile Phe Leu Gly Met Ala Ala Ile His His Gly Asp Arg Pro Ile
 245 250 255

Cys

<110> 17
 <111> 223
 <112> PRT
 <113> Helicobacter pylori

<400> 17
 Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
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 Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
 20 25 30
 Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
 35 40 45
 Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
 50 55 60
 Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Glu Thr Asp
 65 70 75 80
 Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
 85 90 95
 Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
 100 105 110
 Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Gln
 115 120 125
 Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Glu Gln Pro Phe
 130 135 140
 Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
 145 150 155 160

Gly Gln Ala Pro Glu Ile Tyr Val Ala Gly Gly Gly Trp Pro Glu Val
210 215 220

Arg Gln Glu Ala Glu Arg Leu Leu Ala Val Thr Gly Ala Ala Phe Gly
225 230 235 240

Ala Thr Pro Gln Pro Thr Tyr Leu Asp Ser Pro Val Leu Asp Gly Leu
245 250 255

Ala Ala Leu Ala Ala Gln Gly Ala Pro Thr Ala
260 265

<210> 19

<211> 777

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(774)

<400> 19

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Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
1 5 10 15

tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
20 25 30

cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat 144
His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
35 40 45

cac tcc ggg ctt atg ttt gaa cag ata gat ggc att att att tcg tca 192
His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
50 55 60

gta gtg ccg cca atc atg ttt gcg tta gaa aga atg tgc aca aaa tac 240
Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
65 70 75 80

ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa acc ggt tta 288
Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
85 90 95

aat ata aaa tat gac aat ccg aaa gaa gta ggg gca gac aga atc gta 336
Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
100 105 110

aat gct gtc gct gcg ata cac ttg tac ggc aat cca tta att gtt gtc 384
Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
115 120 125

gat ttc gga acc gcc aca acg tac tgc tat att gat gaa aac aaa caa 432
Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
130 135 140

tac atg ggc ggg gcg att gcc cct ggg att aca att tcg aca gag gcg 480
Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145 150 155 160

ctt tac tcg cgt gca gca aag ctt cct cgt atc gaa atc acc cgg ccc 528

Leu	Tyr	Ser	Arg	Ala	Ala	Lys	Leu	Pro	Arg	Ile	Glu	Ile	Thr	Arg	Pro	
				165					170					175		
gac	aat	att	atc	gga	aaa	aac	act	gtt	agc	gcg	atg	caa	tct	gga	att	576
Asp	Asn	Ile	Ile	Gly	Lys	Asn	Thr	Val	Ser	Ala	Met	Gln	Ser	Gly	Ile	
			180					185					190			
tta	ttt	ggc	tat	gtc	ggc	caa	gtg	gaa	gga	atc	gtt	aag	cga	atg	aaa	624
Leu	Phe	Gly	Tyr	Val	Gly	Gln	Val	Glu	Gly	Ile	Val	Lys	Arg	Met	Lys	
		195					200					205				
tgg	cag	gca	aaa	cag	gac	ctc	aag	gtc	att	gcg	aca	gga	ggc	ctg	gcg	672
Trp	Gln	Ala	Lys	Gln	Asp	Leu	Lys	Val	Ile	Ala	Thr	Gly	Gly	Leu	Ala	
	210					215					220					
ccg	ctc	att	gcg	aac	gaa	tca	gat	tgt	ata	gac	atc	gtt	gat	cca	ttc	720
Pro	Leu	Ile	Ala	Asn	Glu	Ser	Asp	Cys	Ile	Asp	Ile	Val	Asp	Pro	Phe	
225				230						235					240	
tta	acc	cta	aaa	ggg	ctg	gaa	ttg	att	tat	gaa	aga	aac	cgc	gta	gga	768
Leu	Thr	Leu	Lys	Gly	Leu	Glu	Leu	Ile	Tyr	Glu	Arg	Asn	Arg	Val	Gly	
				245				250						255		
agt	gta	tag														777
Ser	Val															

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 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(957)

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Met	Lys	Asn	Lys	Glu	Leu	Asn	Leu	His	Thr	Leu	Tyr	Thr	Gln	His	Asn	
1				5					10					15		
egg	gag	tct	tgg	tct	ggt	ttt	ggg	ggg	cat	ttg	tgg	att	gct	gta	tct	96
Arg	Glu	Ser	Trp	Ser	Gly	Phe	Gly	Gly	His	Leu	Ser	Ile	Ala	Val	Ser	
			20				25						30			
gaa	gaa	gag	gca	aaa	gct	gtg	gaa	gga	ttg	aat	gat	tat	cta	tct	gtt	144
Glu	Glu	Glu	Ala	Lys	Ala	Val	Glu	Gly	Leu	Asn	Asp	Tyr	Leu	Ser	Val	
			35			40						45				
gaa	gaa	gtg	gag	acg	atc	tat	att	ccg	ctt	gtt	cgc	ttg	ctt	cat	tta	192
Glu	Glu	Val	Glu	Thr	Ile	Tyr	Ile	Pro	Leu	Val	Arg	Leu	Leu	His	Leu	
	50				55					60						
cat	gtc	aag	tct	gcg	gct	gaa	cgc	aat	aag	cat	gtc	aat	gtt	ttt	ttg	240
His	Val	Lys	Ser	Ala	Ala	Glu	Arg	Asn	Lys	His	Val	Asn	Val	Phe	Leu	
65				70				75						80		
aag	cac	cca	cat	tca	gcc	aaa	att	ccg	ttt	att	atc	ggc	att	gcc	ggc	288
Lys	His	Pro	His	Ser	Ala	Lys	Ile	Pro	Phe	Ile	Ile	Gly	Ile	Ala	Gly	
				85				90						95		

agt gtc gca gtc gga aaa agc acg acg gcg cgg atc ttg cag aag ctg	336
Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu	
100 105 110	
ctt tcg cgt ttg cct gac cgt cca aaa gtg agc ctt atc acg aca gat	384
Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp	
115 120 125	
ggc ttt tta ttt cct act gcc gag ctg aaa aag aaa aat atg atg tca	432
Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser	
130 135 140	
aga aaa gga ttt cct gaa agc tat gat gta aag gcg ctg ctc gaa ttt	480
Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe	
145 150 155 160	
ttg aat gac tta aaa tca gga aag gac agc gta aag gcc ccg gtg tat	528
Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr	
165 170 175	
tcg cat cta acc tat gac cgc gag gaa ggt gtg ttc gag gtt gta gaa	576
Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu	
180 185 190	
cag gcg gat att gtg att att gaa gcc att aat gtt ctt cag tcg ccc	624
Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro	
195 200 205	
acc ttg gag gat gac cgg gaa aac ccg cgt att ttt gtt tcc gat ttc	672
Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe	
210 215 220	
ttt gat ttt tcg att tat gtg gat gcg gag gaa agc cgg att ttc act	720
Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr	
225 230 235 240	
tgg tat tta gag cgt ttt cgc ctg ctt cgg gaa aca gct ttt caa aat	768
Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn	
245 250 255	
cct gat tca tat ttt cat aaa ttt aaa gac ttg tcc gat cag gag gct	816
Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala	
260 265 270	
gac gag atg gca gcc tcg att tgg gag agt gtc aac cgg ccg aat tta	864
Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu	
275 280 285	
tat gaa aat att ttg cca act aaa ttc agg tca gat ctc att ttg cgt	912
Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg	
290 295 300	
aag gga gac ggg cat aag gtc gag gaa gtg ttg gta agg agg gta tga	960
Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val	
305 310 315	

<210> 21

<211> 882

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(379)

<400> 21

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Met	Ser	Ile	Ala	Val	Ser	Glu	Glu	Glu	Ala	Lys	Ala	Val	Glu	Gly	Leu	
1				5					10					15		
aat	gat	tat	cta	tct	gtt	gaa	gaa	gtg	gag	acg	atc	tat	att	ccg	ctt	96
Asn	Asp	Tyr	Leu	Ser	Val	Glu	Glu	Val	Glu	Thr	Ile	Tyr	Ile	Pro	Leu	
			20					25					30			
gtt	cgc	ttg	ctt	cat	tta	cat	gtc	aag	tct	gcg	gct	gaa	cgc	aat	aag	144
Val	Arg	Leu	Leu	His	Leu	His	Val	Lys	Ser	Ala	Ala	Glu	Arg	Asn	Lys	
		35					40					45				
cat	gtc	aat	gtt	ttt	ttg	aag	cac	cca	cat	tca	gcc	aaa	att	ccg	ttt	192
His	Val	Asn	Val	Phe	Leu	Lys	His	Pro	His	Ser	Ala	Lys	Ile	Pro	Phe	
	50					55					60					
att	atc	ggc	att	gcc	ggc	agt	gtc	gca	gtc	gga	aaa	agc	acg	acg	gcg	240
Ile	Ile	Gly	Ile	Ala	Gly	Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	
65					70					75					80	
cgg	atc	ttg	cag	aag	ctg	ctt	tcg	cgt	ttg	cct	gac	cgt	cca	aaa	gtg	288
Arg	Ile	Leu	Gln	Lys	Leu	Leu	Ser	Arg	Leu	Pro	Asp	Arg	Pro	Lys	Val	
			85					90						95		
agc	ctt	atc	acg	aca	gat	ggt	ttt	tta	ttt	cct	act	gcc	gag	ctg	aaa	336
Ser	Leu	Ile	Thr	Thr	Asp	Gly	Phe	Leu	Phe	Pro	Thr	Ala	Glu	Leu	Lys	
			100					105					110			
aag	aaa	aat	atg	atg	tca	aga	aaa	gga	ttt	cct	gaa	agc	tat	gat	gta	384
Lys	Lys	Asn	Met	Met	Ser	Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asp	Val	
		115					120					125				
aag	gcg	ctg	ctc	gaa	ttt	ttg	aat	gac	tta	aaa	tca	gga	aag	gac	agc	432
Lys	Ala	Leu	Leu	Glu	Phe	Leu	Asn	Asp	Leu	Lys	Ser	Gly	Lys	Asp	Ser	
	130					135					140					
gta	aag	gcc	ccg	gtg	tat	tcc	cat	cta	acc	tat	gac	cgc	gag	gaa	ggt	480
Val	Lys	Ala	Pro	Val	Tyr	Ser	His	Leu	Thr	Tyr	Asp	Arg	Glu	Glu	Gly	
145					150					155					160	
gtg	ttc	gag	gtt	gta	gaa	cag	gcg	gat	att	gtg	att	att	gaa	ggc	att	528
Val	Phe	Glu	Val	Val	Glu	Gln	Ala	Asp	Ile	Val	Ile	Ile	Glu	Gly	Ile	
				165					170					175		
aat	gtt	ctt	cag	tcg	ccc	acc	ttg	gag	gat	gac	cgg	gaa	aac	ccg	cgt	576
Asn	Val	Leu	Gln	Ser	Pro	Thr	Leu	Glu	Asp	Asp	Arg	Glu	Asn	Pro	Arg	
			180					185					190			
att	ttt	gtt	tcc	gat	ttc	ttt	gat	ttt	tcg	att	tat	gtg	gat	gcg	gag	624
Ile	Phe	Val	Ser	Asp	Phe	Phe	Asp	Phe	Ser	Ile	Tyr	Val	Asp	Ala	Glu	
		195					200					205				
gaa	agc	cgg	att	ttc	act	tgg	tat	tta	gag	cgt	ttt	cgc	ctg	ctt	cgg	672
Glu	Ser	Arg	Ile	Phe	Thr	Trp	Tyr	Leu	Glu	Arg	Phe	Arg	Leu	Leu	Arg	
	210					215					220					

gaa aca gct ttt caa aat cct gat tca tat ttt cat aaa ttt aaa gac 720
 Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
 225 230 235 240
 ttg tcc gat cag gag gct gac gag atg gca gcc tcg att tgg gag agt 768
 Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
 245 250 255
 gtc aac cgg ccg aat tta tat gaa aat att ttg cca act aaa ttc agg 816
 Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg
 260 265 270
 tca gat ctg att ttg cgt aag gga gac ggg cat aag gtc gag gaa gtg 864
 Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val
 275 280 285
 ttg gta agg agg gta tga 882
 Leu Val Arg Arg Val
 290

<210> 22
 <211> 346
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(843)

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 1 5 10 15
 tat att ccg ctt gtt cgc ttg ctt cat tta cat gtc aag tct gcg gct 96
 Tyr Ile Pro Leu Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala
 20 25 30
 gaa cgc aat aag cat gtc aat gtt ttt ttg aag cac cca cat tca gcc 144
 Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala
 35 40 45
 aaa att ccg ttt att atc ggc att gcc ggc agt gtc gca gtc gga aaa 192
 Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys
 50 55 60
 agc acg acg gcg cgg atc ttg cag aag ctg ctt tcg cgt ttg cct gac 240
 Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp
 65 70 75 80
 cgt cca aaa gtg agc ctt atc acg aca gat ggt ttt tta ttt cct act 288
 Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr
 85 90 95
 gcc gag ctg aaa aag aaa aat atg atg tca aga aaa gga ttt cct gaa 336
 Ala Glu Leu Lys Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Glu
 100 105 110
 agc tat gat gta aag gcg ctg ctg gaa ttt ttg aat gac tta aaa tca 384

Ser	Tyr	Asp	Val	Lys	Ala	Leu	Leu	Glu	Phe	Leu	Asn	Asp	Leu	Lys	Ser		
		115					120					125					
gga	aag	gac	agc	gta	aag	gcc	ccg	gtg	tat	tcc	cat	cta	acc	tat	gac		432
Gly	Lys	Asp	Ser	Val	Lys	Ala	Pro	Val	Tyr	Ser	His	Leu	Thr	Tyr	Asp		
	130					135					140						
cgc	gag	gaa	ggt	gtg	ttc	gag	gtt	gta	gaa	cag	gcg	gat	att	gtg	att		480
Arg	Glu	Glu	Gly	Val	Phe	Glu	Val	Val	Glu	Gln	Ala	Asp	Ile	Val	Ile		
145					150					155					160		
att	gaa	ggc	att	aat	gtt	ctt	cag	tgc	ccc	acc	ttg	gag	gat	gac	cgg		528
Ile	Glu	Gly	Ile	Asn	Val	Leu	Gln	Ser	Pro	Thr	Leu	Glu	Asp	Asp	Arg		
				165					170					175			
gaa	aac	ccg	cgt	att	ttt	gtt	tcc	gat	ttc	ttt	gat	ttt	tgc	att	tat		576
Glu	Asn	Pro	Arg	Ile	Phe	Val	Ser	Asp	Phe	Phe	Asp	Phe	Ser	Ile	Tyr		
			180					185					190				
gtg	gat	gcg	gag	gaa	agc	cgg	att	ttc	act	tgg	tat	tta	gag	cgt	ttt		624
Val	Asp	Ala	Glu	Glu	Ser	Arg	Ile	Phe	Thr	Trp	Tyr	Leu	Glu	Arg	Phe		
	195					200						205					
cgc	ctg	ctt	cgg	gaa	aca	gct	ttt	caa	aat	cct	gat	tca	tat	ttt	cat		672
Arg	Leu	Leu	Arg	Glu	Thr	Ala	Phe	Gln	Asn	Pro	Asp	Ser	Tyr	Phe	His		
	210					215					220						
aaa	ttt	aaa	gac	ttg	tcc	gat	cag	gag	gct	gac	gag	atg	gca	gcc	tgc		720
Lys	Phe	Lys	Asp	Leu	Ser	Asp	Gln	Glu	Ala	Asp	Glu	Met	Ala	Ala	Ser		
225					230					235				240			
att	tgg	gag	agt	gtc	aac	cgg	ccg	aat	tta	tat	gaa	aat	att	ttg	cca		768
Ile	Trp	Glu	Ser	Val	Asn	Arg	Pro	Asn	Leu	Tyr	Glu	Asn	Ile	Leu	Pro		
				245					250					255			
act	aaa	ttc	agg	tca	gat	ctc	att	ttg	cgt	aag	gga	gac	ggg	cat	aag		816
Thr	Lys	Phe	Arg	Ser	Asp	Leu	Ile	Leu	Arg	Lys	Gly	Asp	Gly	His	Lys		
			260					265					270				
gtc	gag	gaa	gtg	ttg	gta	agg	agg	gta	tga								846
Val	Glu	Glu	Val	Leu	Val	Arg	Arg	Val									
	275					280											

<210> 23
 <211> 831
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(831)

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Met	Lys	Thr	Lys	Leu	Asp	Phe	Leu	Lys	Met	Lys	Glu	Ser	Glu	Glu	Pro		
1				5				10					15				
att	gtc	atg	ctg	acc	gct	tat	gat	tat	ccg	gca	gct	aaa	ctt	gct	gaa		96
Ile	Val	Met	Leu	Thr	Ala	Tyr	Asp	Tyr	Pro	Ala	Ala	Lys	Leu	Ala	Glu		
			20			25							30				

caa gcg gga gtt gac atg att tta gtc ggt gat tca ctt gga atg gtc	144
Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val	
35 40 45	
gtc ctc ggc ctt gat tca act gtc ggt gtg aca gtt gcg gac atg atc	192
Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile	
50 55 60	
cat cat aca aaa gcc gtt aaa agg ggt gcg ccg aat acc ttt att gtg	240
His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val	
55 70 75 80	
aca gat atg ccg ttt atg tct tat cac ctg tct aag gaa gat acg ctg	288
Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu	
85 90 95	
aaa aat gca gcg gct atc gtt cag gaa agc gga gct gac gca ctg aag	336
Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys	
100 105 110	
ctt gag ggc gga gaa ggc gtg ttc gaa tcc att cgc gca ttg acg ctt	384
Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu	
115 120 125	
gga ggc att cca gta gtc agt cac tta ggt ttg aca ccg cag tca gtc	432
Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val	
130 135 140	
ggc gta ctg ggc ggc tat aaa gta cag ggc aaa gac gaa caa agc gcc	480
Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala	
145 150 155 160	
aaa aaa tta ata gaa gac agt ata aaa tgc gaa gaa gca gga gct atg	528
Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met	
165 170 175	
atg ctt gtg ctg gaa tgt gtg ccg gca gaa ctc aca gcc aaa att gcc	576
Met Leu Val Leu Glu Cys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala	
180 185 190	
gag acg cta agc ata ccg gtc att gga atc ggg gct ggt gtg aaa gcg	624
Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala	
195 200 205	
gac gga caa gtt ctc gtt tat cat gat att atc ggc cac ggt gtt gag	672
Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Glu	
210 215 220	
aga aca cct aaa ttt gta aag caa tat acg cgc att gat gaa acc atc	720
Arg Thr Pro Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile	
225 230 235 240	
gaa aca gca atc agc gga tat gtt cag gat gta aga cat cgt gct ttc	768
Glu Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Phe	
245 250 255	
cct gaa caa aag cat tcc ttt caa atg aac cag aca gtg ctt gac ggc	816
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly	
260 265 270	

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 Leu Tyr Gly Gly Lys
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<210> 24
 <211> 277
 <212> PRT
 <213> Bacillus subtilis

<400> 24

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Ile	Val	Met	Leu	Thr	Ala	Tyr	Asp	Tyr	Pro	Ala	Ala	Lys	Leu	Ala	Glu
			20					25						30	
Gln	Ala	Gly	Val	Asp	Met	Ile	Leu	Val	Gly	Asp	Ser	Leu	Gly	Met	Val
		35					40					45			
Val	Leu	Gly	Leu	Asp	Ser	Thr	Val	Gly	Val	Thr	Val	Ala	Asp	Met	Ile
	50					55					60				
His	His	Thr	Lys	Ala	Val	Lys	Arg	Gly	Ala	Pro	Asn	Thr	Phe	Ile	Val
65					70					75					80
Thr	Asp	Met	Pro	Phe	Met	Ser	Tyr	His	Leu	Ser	Lys	Glu	Asp	Thr	Leu
				85					90					95	
Lys	Asn	Ala	Ala	Ala	Ile	Val	Gln	Glu	Ser	Gly	Ala	Asp	Ala	Leu	Lys
			100					105					110		
Leu	Glu	Gly	Gly	Glu	Gly	Val	Phe	Glu	Ser	Ile	Arg	Ala	Leu	Thr	Leu
		115					120					125			
Gly	Gly	Ile	Pro	Val	Val	Ser	His	Leu	Gly	Leu	Thr	Pro	Gln	Ser	Val
	130					135					140				
Gly	Val	Leu	Gly	Gly	Tyr	Lys	Val	Gln	Gly	Lys	Asp	Glu	Gln	Ser	Ala
145					150					155					160
Lys	Lys	Leu	Ile	Glu	Asp	Ser	Ile	Lys	Cys	Glu	Glu	Ala	Gly	Ala	Met
			165					170						175	
Met	Leu	Val	Leu	Glu	Cys	Val	Pro	Ala	Glu	Leu	Thr	Ala	Lys	Ile	Ala
		180						185					190		
Glu	Thr	Leu	Ser	Ile	Pro	Val	Ile	Gly	Ile	Gly	Ala	Gly	Val	Lys	Ala
		195					200					205			
Asp	Gly	Gln	Val	Leu	Val	Tyr	His	Asp	Ile	Ile	Gly	His	Gly	Val	Glu
	210					215					220				
Arg	Thr	Pro	Lys	Phe	Val	Lys	Gln	Tyr	Thr	Arg	Ile	Asp	Glu	Thr	Ile
225					230					235					240
Glu	Thr	Ala	Ile	Ser	Gly	Tyr	Val	Gln	Asp	Val	Arg	His	Arg	Ala	Phe
			245						250					255	
Pro	Glu	Gln	Lys	His	Ser	Phe	Gln	Met	Asn	Gln	Thr	Val	Leu	Asp	Gly
		260						265					270		

Leu Tyr Gly Gly Lys
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<210> 25

<211> 853

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(853)

<400> 25

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1 5 10 15	
tac cat tca gag ggc aag tca atc gga ttt gtt ccg acg atg ggg ttt	96
Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe	
20 25 30	
ctg cat gag ggg cat tta acc tta gca gac aaa gca aga caa gaa aac	144
Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn	
35 40 45	
gac gcc gtt att atg agt att ttt gtg aat cct gca caa ttc ggc cct	192
Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro	
50 55 60	
aat gaa gat ttt gaa gca tat ccg cgc gat att gag cgg gat gca gct	240
Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala	
65 70 75 80	
ctt gca gaa aac gcc gga gtc gat att ctt ttt acg cca gat gct cat	288
Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His	
85 90 95	
gat atg tat ccc ggt gaa aag aat gtc acg att cat gta gaa aga cgc	336
Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg	
100 105 110	
aca gac gtg tta tgc ggg cgc tca aga gaa gga cat ttt gac ggg gtc	384
Thr Asp Val Leu Cys Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val	
115 120 125	
gcg atc gta ctg acg aag ctt ttc aat cta gtc aag ccg act cgt gcc	432
Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala	
130 135 140	
tat ttc ggt tta aaa gat gcg cag cag gta gct gtt gtt gat ggg tta	480
Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu	
145 150 155 160	
atc agc gac ttc ttc atg gat att gaa ttg gtt cct gtc gat acg gtc	528
Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val	
165 170 175	
aga gag gaa gac ggc tta gcc aaa agc tct cgc aat gta tac tta aca	576
Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr	

	180		185		190	
	gct gag gaa aga aaa gaa gcg cct aag ctg tat cgg gcc ctt caa aca					624
	Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr					
	195		200		205	
	agt gcg gaa ctt gtc caa gcc ggt gaa aga gat cct gaa gcg gtg ata					672
	Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile					
	210		215		220	
	aaa gct gca aaa gat atc att gaa acg act agc gga acc ata gac tat					720
	Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr					
	225		230		235	240
	gta gag ctt tat tcc tat ccg gaa ctc gag cct gtg aat gaa att gct					768
	Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala					
		245		250		255
	gga aag atg att ctc gct gtt gca gtt gct ttt tca aaa gcg cgt tta					816
	Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu					
		260		265		270
	ata gat aat atc att att gat att cga gaa atg gag aga ata					853
	Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile					
	275		280		285	

<210> 26

<211> 286

<212> PRT

<213> Bacillus subtilis

<400> 26

Met	Arg	Gln	Ile	Thr	Asp	Ile	Ser	Gln	Leu	Lys	Glu	Ala	Ile	Lys	Gln
1				5					10					15	
Tyr	His	Ser	Glu	Gly	Lys	Ser	Ile	Gly	Phe	Val	Pro	Thr	Met	Gly	Phe
			20					25					30		
Leu	His	Glu	Gly	His	Leu	Thr	Leu	Ala	Asp	Lys	Ala	Arg	Gln	Glu	Asn
		35					40					45			
Asp	Ala	Val	Ile	Met	Ser	Ile	Phe	Val	Asn	Pro	Ala	Gln	Phe	Gly	Pro
	50					55					60				
Asn	Glu	Asp	Phe	Glu	Ala	Tyr	Pro	Arg	Asp	Ile	Glu	Arg	Asp	Ala	Ala
65					70				75					80	
Leu	Ala	Glu	Asn	Ala	Gly	Val	Asp	Ile	Leu	Phe	Thr	Pro	Asp	Ala	His
			85					90					95		
Asp	Met	Tyr	Pro	Gly	Glu	Lys	Asn	Val	Thr	Ile	His	Val	Glu	Arg	Arg
			100					105					110		
Thr	Asp	Val	Leu	Cys	Gly	Arg	Ser	Arg	Glu	Gly	His	Phe	Asp	Gly	Val
		115					120					125			
Ala	Ile	Val	Leu	Thr	Lys	Leu	Phe	Asn	Leu	Val	Lys	Pro	Thr	Arg	Ala
	130					135					140				
Tyr	Phe	Gly	Leu	Lys	Asp	Ala	Gln	Gln	Val	Ala	Val	Val	Asp	Gly	Leu

145		150		155		160
Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val						
		165		170		175
Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr						
		180		185		190
Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr						
		195		200		205
Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile						
		210		215		220
Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr						
		225		230		235
Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala						
		245		250		255
Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu						
		260		265		270
Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile						
		275		280		285

<210> 27

<211> 381

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(331)

<400> 27

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Met Tyr Arg Thr Met Met Ser Gly Lys Leu His Arg Ala Thr Val Thr	
1 5 10 15	
gaa gca aac ctg aac tat gtg gga agc att aca att gat gaa gat ctc	96
Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu	
20 25 30	
att gat gct gtg gga atg ctt cct aat gaa aaa gta caa att gtg aat	144
Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn	
35 40 45	
aat aat aat gga gca cgt ctt gaa acg tat att att cct ggt aaa cgg	192
Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile Ile Pro Gly Lys Arg	
50 55 60	
gga agc ggc gtc ata tgc tta aac ggt gca gcc gca cgc ctt gtg cag	240
Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala Ala Arg Leu Val Gln	
65 70 75 80	
gaa gga gat aag gtc att att att tcc tac aaa atg atg tct gat caa	288
Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln	
85 90 95	

aaa att gaa caa atg ctg ggg aac gaa cca gcc cgt aca att ttg 381
Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
115 120 125

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<400> 28
Met Tyr Arg Thr Met Met Ser Gly Lys Leu His Arg Ala Thr Val Thr
  1             5             10             15
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Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn
35 40 45

Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala Ala Arg Leu Val Gln
55 70 75 80

Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
85 90 95

Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
100 105 110

Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
115 120 125

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<210> 29
<211> 894
<212> DNA
<213> Bacillus subtilis
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<220>
<221> CDS
<222> (1) .. (894)
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<400> 29
atg aaa att gga att atc ggc gga ggc tcc gtt ggt ctt tta tgc gcc      48
Met Lys Ile Gly Ile Ile Gly Gly Gly Ser Val Gly Leu Leu Cys Ala
      1              5              10              15
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tat	tat	ttg	tca	ctt	tat	cac	gac	gtg	act	gtt	gtg	acg	agg	cgg	caa	96
Tyr	Tyr	Leu	Ser	Leu	Tyr	His	Asp	Val	Thr	Val	Val	Thr	Arg	Arg	Gln	
		20						25					30			

gaa cag gct gcg gcc att cag tct gaa gga atc cgg ctt tat aaa ggc 144
Glu Gln Ala Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly
35 40 45

ggg gag gaa ttc agg gct gat tgc agt gcg gac acg agt atc aat tcg	192
Gly Glu Glu Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser	
50 55 60	
gac ttt gac ctg ctt gtc gtg aca gtg aag cag cat cag ctt caa tct	240
Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser	
65 70 75 80	
gtt ttt tcg tcg ctt gaa cga atc ggg aag acg aat ata tta ttt ttg	288
Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu	
85 90 95	
caa aac ggc atg ggg cat atc cac gac cta aaa gac tgg cac gtt ggc	336
Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly	
100 105 110	
cat tcc att tat gtt gga atc gtt gag cac gga gct gta aga aaa tcg	384
His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser	
115 120 125	
gat aca gct gtt gat cat aca ggc cta ggt gcg ata aaa tgg agc gcg	432
Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala	
130 135 140	
ttc gac gat gct gaa cca gac cgg ctg aac atc ttg ttt cag cat aac	480
Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn	
145 150 155 160	
cat tcg gat ttt ccg att tat tat gag acg gat tgg tac cgt ctg ctg	528
His Ser Asp Phe Pro Ile Tyr Tyr Glu Thr Asp Trp Tyr Arg Leu Leu	
165 170 175	
acg ggc aag ctg att gta aat gcg tgt att aat cct tta act gcg tta	576
Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu	
180 185 190	
ttg caa gtg aaa aat gga gaa ctg ctg aca acg cca gct tat ctg gct	624
Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala	
195 200 205	
ttt atg aag ctg gta ttt cag gag gca tgc cgc att tta aaa ctt gaa	672
Phe Met Lys Leu Val Phe Gln Glu Ala Cys Arg Ile Leu Lys Leu Glu	
210 215 220	
aat gaa gaa aag gct tgg gag cgg gtt cag gcc gtt tgt ggg caa acg	720
Asn Glu Glu Lys Ala Trp Glu Arg Val Gln Ala Val Cys Gly Gln Thr	
225 230 235 240	
aaa gag aat cgt tca tca atg ctg gtt gac gtc att gga ggc cgg cag	768
Lys Glu Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Gln	
245 250 255	
acg gaa gct gac gcc att atc gga tac tta ttg aag gaa gca agt ctt	816
Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu	
260 265 270	
caa ggt ctt gat gcc gtc cac cta gag ttt tta tat ggc agc atc aaa	864
Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys	
275 280 285	

894

<400> 30

Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu
260 265 270

Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
 275 280 285

Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
 290 295

<210> 31

<211> 1725

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1722)

<400> 31

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1 5 10 15	
acg atg agc gga gca tta atg ctg att gaa tca tta aaa aaa gag aaa	96
Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys	
20 25 30	
gta gaa atg atc ttc ggt tat ccg ggc ggg gct gtg ctt ccg att tac	144
Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr	
35 40 45	
gat aag cta tac aat tca ggg ttg gta cat atc ctt ccc cgt cac gaa	192
Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu	
50 55 60	
caa gga gca att cat gca gcg gag gga tac gca agg gtc tcc gga aaa	240
Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys	
65 70 75 80	
ccg ggt gtc gtc att gcc acg tca ggg ccg gga gcg aca aac ctt gtt	288
Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val	
85 90 95	
aca ggc ctt gct gat gcc atg att gat tca ttg ccg tta gtc gtc ttt	336
Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe	
100 105 110	
aca ggg cag gta gca acc tct gta atc ggg agc gat gca ttt cag gaa	384
Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Gln Glu	
115 120 125	
gca gac att tta ggg att acg atg cca gta aca aaa cac agc tac cag	432
Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Gln	
130 135 140	
gtt cgc cag ccg gaa gat ctg ccg cgc atc att aaa gaa gcg ttc cat	480
Val Arg Gln Pro Glu Asp Leu Pro Arg Ile Ile Lys Glu Ala Phe His	
145 150 155 160	
att gca aca act gga aga ccc gga cct gta ttg att gat att ccg aaa	528
Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys	
165 170 175	

gat gta gca aca att gaa gga gaa ttc agc tac gat cat gag atg aat	575
Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn	
180 185 190	
ctc ccg gga tac cag ccg aca aca gag ccg aat tat ttg cag atc cgc	624
Leu Pro Gly Tyr Gln Pro Thr Thr Glu Pro Asn Tyr Leu Gln Ile Arg	
195 200 205	
aag ctt gtg gaa gcc gtg agc agt gcg aaa aaa ccg gtg atc ctg gcg	672
Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala	
210 215 220	
ggc gcg ggc gta ctg cac gga aaa gcg tca gaa gaa tta aaa aat tat	720
Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr	
225 230 235 240	
gct gaa cag cag caa atc cct gtg gca cac acc ctt ttg ggg ctc gga	768
Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly	
245 250 255	
ggc ttc ccg gct gac cat ccg ctt ttc cta ggg atg gcg gga atg cac	816
Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His	
260 265 270	
ggc act tat aca gcc aat atg gcc ctt cat gaa tgt gat cta tta atc	864
Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile	
275 280 285	
agt atc ggc gcc cgt ttt gat gac cgt gtc aca gga aac ctg aaa cac	912
Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His	
290 295 300	
ttt gcc aga aac gca aag ata gcc cac atc gat att gat cca gct gaa	960
Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu	
305 310 315 320	
atc gga aaa atc atg aaa aca cag att cct gta gtc gga gac agc aaa	1008
Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys	
325 330 335	
att gtc ctg cag gag ctg atc aaa caa gac ggc aaa caa agc gat tca	1056
Ile Val Leu Gln Glu Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser	
340 345 350	
agc gaa tgg aaa aaa cag ctc gca gaa tgg aaa gaa gag tat ccg ctc	1104
Ser Glu Trp Lys Lys Gln Leu Ala Glu Trp Lys Glu Glu Tyr Pro Leu	
355 360 365	
tgg tat gta gat aat gaa gaa gaa ggt ttt aaa cct cag aaa ttg att	1152
Trp Tyr Val Asp Asn Glu Glu Glu Gly Phe Lys Pro Gln Lys Leu Ile	
370 375 380	
gaa tat att cat caa ttt aca aaa gga gag gcc att gtc gca acg gat	1200
Glu Tyr Ile His Gln Phe Thr Lys Gly Glu Ala Ile Val Ala Thr Asp	
385 390 395 400	
gta ggc cag cat caa atg tgg tca gcg caa ttt tat ccg ttc caa aaa	1248
Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys	
405 410 415	

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<400> 32
Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Glu Cys Thr Gln
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                20                      25                      30

Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
      35                      40                      45

Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu
      50                      55                      60

Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
      65                      70                      75                      80

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Pro	Gly	Val	Val	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	85	90	95	
Thr	Gly	Leu	Ala	Asp	Ala	Met	Ile	Asp	Ser	Leu	Pro	Leu	Val	Val	Phe	100	105	110	
Thr	Gly	Gln	Val	Ala	Thr	Ser	Val	Ile	Gly	Ser	Asp	Ala	Phe	Gln	Glu	115	120	125	
Ala	Asp	Ile	Leu	Gly	Ile	Thr	Met	Pro	Val	Thr	Lys	His	Ser	Tyr	Gln	130	135	140	
Val	Arg	Gln	Pro	Glu	Asp	Leu	Pro	Arg	Ile	Ile	Lys	Glu	Ala	Phe	His	145	150	155	160
Ile	Ala	Thr	Thr	Gly	Arg	Pro	Gly	Pro	Val	Leu	Ile	Asp	Ile	Pro	Lys	165	170	175	
Asp	Val	Ala	Thr	Ile	Glu	Gly	Glu	Phe	Ser	Tyr	Asp	His	Glu	Met	Asn	180	185	190	
Leu	Pro	Gly	Tyr	Gln	Pro	Thr	Thr	Glu	Pro	Asn	Tyr	Leu	Gln	Ile	Arg	195	200	205	
Lys	Leu	Val	Glu	Ala	Val	Ser	Ser	Ala	Lys	Lys	Pro	Val	Ile	Leu	Ala	210	215	220	
Gly	Ala	Gly	Val	Leu	His	Gly	Lys	Ala	Ser	Glu	Glu	Leu	Lys	Asn	Tyr	225	230	235	240
Ala	Glu	Gln	Gln	Gln	Ile	Pro	Val	Ala	His	Thr	Leu	Leu	Gly	Leu	Gly	245	250	255	
Gly	Phe	Pro	Ala	Asp	His	Pro	Leu	Phe	Leu	Gly	Met	Ala	Gly	Met	His	260	265	270	
Gly	Thr	Tyr	Thr	Ala	Asn	Met	Ala	Leu	His	Glu	Cys	Asp	Leu	Leu	Ile	275	280	285	
Ser	Ile	Gly	Ala	Arg	Phe	Asp	Asp	Arg	Val	Thr	Gly	Asn	Leu	Lys	His	290	295	300	
Phe	Ala	Arg	Asn	Ala	Lys	Ile	Ala	His	Ile	Asp	Ile	Asp	Pro	Ala	Glu	305	310	315	320
Ile	Gly	Lys	Ile	Met	Lys	Thr	Gln	Ile	Pro	Val	Val	Gly	Asp	Ser	Lys	325	330	335	
Ile	Val	Leu	Gln	Glu	Leu	Ile	Lys	Gln	Asp	Gly	Lys	Gln	Ser	Asp	Ser	340	345	350	
Ser	Glu	Trp	Lys	Lys	Gln	Leu	Ala	Glu	Trp	Lys	Glu	Glu	Tyr	Pro	Leu	355	360	365	
Trp	Tyr	Val	Asp	Asn	Glu	Glu	Glu	Gly	Phe	Lys	Pro	Gln	Lys	Leu	Ile	370	375	380	
Glu	Tyr	Ile	His	Gln	Phe	Thr	Lys	Gly	Glu	Ala	Ile	Val	Ala	Thr	Asp	385	390	395	400

Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys
 405 410 415
 Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly
 420 425 430
 Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Glu Lys Asp Ala Thr Val
 435 440 445
 Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu
 450 455 460
 Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn
 465 470 475 480
 Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu
 485 490 495
 Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys
 500 505 510
 Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala
 515 520 525
 Glu Ala Lys Glu Lys Leu Glu Glu Ala Leu Thr Ser Arg Glu Pro Val
 530 535 540
 Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val
 545 550 555 560
 Ala Pro Gly Lys Gly Leu His Glu Met Val Gly Val Lys Pro
 565 570

<210> 33
 <211> 525
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(522)

<400> 33
 ttg aaa aga att atc aca ttg act gtg gtg aac cgc tcc ggg gtg tta 48
 Met Lys Arg Ile Ile Thr Leu Thr Val Val Asn Arg Ser Gly Val Leu
 1 5 10 15
 aac cgg atc acc ggt cta ttc aca aaa agg cat tac aac att gaa agc 96
 Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser
 20 25 30
 att aca gtt gga cac aca gaa aca gcc ggc gtt tcc aga atc acc ttc 144
 Ile Thr Val Gly His Thr Glu Thr Ala Gly Val Ser Arg Ile Thr Phe
 35 40 45
 gtc gtt cat gtt gaa ggt gaa aat gat gtt gaa cag tta acg aaa cag 192
 Val Val His Val Glu Gly Glu Asn Asp Val Glu Gln Leu Thr Lys Gln
 50 55 60
 ctc aac aaa cag att gat gtg ctg aaa gtc aca gac atc aca aat caa 240

Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln
 65 70 75 80
 tcg att gtc cag agg gag ctg gcc tta atc aag gtt gtc tcc gca cct 288
 Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro
 85 90 95
 tca aca aga aca gag att aat gga atc ata gaa ccg ttt aga gcc tct 336
 Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser
 100 105 110
 gtc gtt gat gtc agc aga gac agc atc gtt gtt cag gtg aca ggt gaa 384
 Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu
 115 120 125
 tct aac aaa att gaa gcg ctt att gag tta tta aaa cct tat ggc att 432
 Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile
 130 135 140
 aaa gaa atc gcg aga aca ggt aca acg gct ttt gcg agg gga acc agc 480
 Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser
 145 150 155 160
 aaa agg cgt cat cca ata aaa caa tat cta ttg tat aaa aca taa 525
 Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
 165 170

<210> 34

<211> 174

<212> PRT

<213> Bacillus subtilis

<400> 34

Met Lys Arg Ile Ile Thr Leu Thr Val Val Asn Arg Ser Gly Val Leu
 1 5 10 15
 Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser
 20 25 30
 Ile Thr Val Gly His Thr Glu Thr Ala Gly Val Ser Arg Ile Thr Phe
 35 40 45
 Val Val His Val Glu Gly Glu Asn Asp Val Glu Gln Leu Thr Lys Gln
 50 55 60
 Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln
 65 70 75 80
 Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro
 85 90 95
 Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser
 100 105 110
 Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu
 115 120 125
 Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile
 130 135 140

Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser
145 150 155 160

Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
165 170

<210> 35

<211> 1029

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1026)

<400> 35

atg gta aaa gta tat tat aac ggt gat atc aaa gag aac gta ttg gct 48
Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
1 5 10 15

gga aaa aca gta gcg gtt atc ggg tac ggt tcg caa ggc cac gca cat 96
Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His
20 25 30

gcc ctg aac ctt aaa gaa agc gga gta gac gtg atc gtc ggt gtt aga 144
Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg
35 40 45

caa gga aaa tct ttc act caa gcc caa gaa gac gga cat aaa gta ttt 192
Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe
50 55 60

tca gta aaa gaa gcg gca gcc caa gcc gaa atc atc atg gtt ctg ctt 240
Ser Val Lys Glu Ala Ala Ala Gln Ala Glu Ile Ile Met Val Leu Leu
65 70 75 80

ccg gat gag cag cag caa aaa gta tac gaa gct gaa atc aaa gat gaa 288
Pro Asp Glu Gln Gln Gln Lys Val Tyr Glu Ala Glu Ile Lys Asp Glu
85 90 95

ttg aca gca gga aaa tca tta gta ttc gct cat gga ttt aac gtg cat 336
Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Gly Phe Asn Val His
100 105 110

ttc cat caa att gtt cct ccg gcg gat gta gat gta ttc tta gtg gcc 384
Phe His Gln Ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala
115 120 125

cct aaa ggc ccg gga cac ttg gta aga aga aca tat gag caa gga gct 432
Pro Lys Gly Pro Gly His Leu Val Arg Arg Thr Tyr Glu Gln Gly Ala
130 135 140

ggc gta cct gca ttg ttc gca atc tat caa gat gtg act gga gaa gca 480
Gly Val Pro Ala Leu Phe Ala Ile Tyr Gln Asp Val Thr Gly Glu Ala
145 150 155 160

aga gac aaa gcc ctc gct tat gct aaa gga atc ggc ggc gca aga gcg 528
Arg Asp Lys Ala Leu Ala Tyr Ala Lys Gly Ile Gly Gly Ala Arg Ala
165 170 175

ggc gta tta gaa acg aca ttt aaa gaa gaa aca gaa aca gat ttg ttc 576
 Gly Val Leu Glu Thr Thr Phe Lys Glu Glu Thr Glu Thr Asp Leu Phe
 180 185 190

ggt gag caa gca gtt ctt tgc ggc gga tta agc gcg ctt gtc aaa gcc 624
 Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Ser Ala Leu Val Lys Ala
 195 200 205

gga ttt gaa acc tta act gaa gca ggt tat cag cct gaa ctt gca tac 672
 Gly Phe Glu Thr Leu Thr Glu Ala Gly Tyr Gln Pro Glu Leu Ala Tyr
 210 215 220

ttc gag tgt ctt cat gag ctg aaa tta atc gta gac ctt atg tac gaa 720
 Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu
 225 230 235 240

gaa gga ctt gca gga atg aga tat tca atc tct gac aca gca cag tgg 768
 Glu Gly Leu Ala Gly Met Arg Tyr Ser Ile Ser Asp Thr Ala Gln Trp
 245 250 255

gga gat ttc gta tca ggc cct cgc gtt gtg gac gcc aaa gta aaa gaa 816
 Gly Asp Phe Val Ser Gly Pro Arg Val Val Asp Ala Lys Val Lys Glu
 260 265 270

tct atg aaa gaa gta tta aaa gat atc caa aac ggt aca ttc gca aaa 864
 Ser Met Lys Glu Val Leu Lys Asp Ile Gln Asn Gly Thr Phe Ala Lys
 275 280 285

gag tgg atc gtc gaa aac caa gta aac cgt cct cgt ttc aac gct atc 912
 Glu Trp Ile Val Glu Asn Gln Val Asn Arg Pro Arg Phe Asn Ala Ile
 290 295 300

aat gca agc gag aac gaa cat caa atc gaa gta gtg gga aga aag ctt 960
 Asn Ala Ser Glu Asn Glu His Gln Ile Glu Val Val Gly Arg Lys Leu
 305 310 315 320

cgt gaa atg atg ccg ttt gtg aaa caa ggc aag aag aag gaa gcg gtg 1008
 Arg Glu Met Met Pro Phe Val Lys Gln Gly Lys Lys Lys Glu Ala Val
 325 330 335

gtc tcc gtt gcg caa aat taa 1029
 Val Ser Val Ala Gln Asn
 340

<210> 35

<211> 342

<212> PRT

<213> Bacillus subtilis

<400> 35

Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
1 5 10 15

Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His
20 25 30

Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg
35 40 45

Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe

50		55		60
Ser Val Lys Glu Ala Ala Ala Gln Ala Glu Ile Ile Met Val Leu Leu				
65		70		75
Pro Asp Glu Gln Gln Gln Lys Val Tyr Glu Ala Glu Ile Lys Asp Glu				
		85		90
Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Gly Phe Asn Val His				
		100		105
Phe His Gln Ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala				
		115		120
Pro Lys Gly Pro Gly His Leu Val Arg Arg Thr Tyr Glu Gln Gly Ala				
		130		135
Gly Val Pro Ala Leu Phe Ala Ile Tyr Gln Asp Val Thr Gly Glu Ala				
		145		150
Arg Asp Lys Ala Leu Ala Tyr Ala Lys Gly Ile Gly Gly Ala Arg Ala				
		165		170
Gly Val Leu Glu Thr Thr Phe Lys Glu Glu Thr Glu Thr Asp Leu Phe				
		180		185
Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Ser Ala Leu Val Lys Ala				
		195		200
Gly Phe Glu Thr Leu Thr Glu Ala Gly Tyr Gln Pro Glu Leu Ala Tyr				
		210		215
Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu				
		225		230
Glu Gly Leu Ala Gly Met Arg Tyr Ser Ile Ser Asp Thr Ala Gln Trp				
		245		250
Gly Asp Phe Val Ser Gly Pro Arg Val Val Asp Ala Lys Val Lys Glu				
		260		265
Ser Met Lys Glu Val Leu Lys Asp Ile Gln Asn Gly Thr Phe Ala Lys				
		275		280
Glu Trp Ile Val Glu Asn Gln Val Asn Arg Pro Arg Phe Asn Ala Ile				
		290		295
Asn Ala Ser Glu Asn Glu His Gln Ile Glu Val Val Gly Arg Lys Leu				
		305		310
Arg Glu Met Met Pro Phe Val Lys Gln Gly Lys Lys Lys Glu Ala Val				
		325		330
Val Ser Val Ala Gln Asn				
		340		

<210> 37

<211> 1674

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1674)

<400> 37

atg gca gaa tta cgc agt aat atg atc aca caa gga atc gat aga gct	48
Met Ala Glu Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala	
1 5 10 15	
ccg cac cgc agt ttg ctt cgt gca gca ggg gta aaa gaa gag gat ttc	96
Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Glu Glu Asp Phe	
20 25 30	
ggc aag ccg ttt att gcg gtg tgt aat tca tac att gat atc gtt ccc	144
Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro	
35 40 45	
ggc cat gtt cac ttg cag gag ttt ggg aaa atc gta aaa gaa gca atc	192
Gly His Val His Leu Gln Glu Phe Gly Lys Ile Val Lys Glu Ala Ile	
50 55 60	
aga gaa gca ggg ggc gtt ccg ttt gaa ttt aat acc att ggg gta gat	240
Arg Glu Ala Gly Gly Val Pro Phe Glu Phe Asn Thr Ile Gly Val Asp	
65 70 75 80	
gat ggc atc gca atg ggg cat atc ggt atg aga tat tgc ctg cca agc	288
Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser	
85 90 95	
cgt gaa att atc gca gac tct gtg gaa acg gtt gta tcc gca cac tgg	336
Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Val Ser Ala His Trp	
100 105 110	
ttt gac gga atg gtc tgt att ccg aac tgc gac aaa atc aca ccg gga	384
Phe Asp Gly Met Val Cys Ile Pro Asn Cys Asp Lys Ile Thr Pro Gly	
115 120 125	
atg ctt atg gcg gca atg cgc atc aac att ccg acg att ttt gtc agc	432
Met Leu Met Ala Ala Met Arg Ile Asn Ile Pro Thr Ile Phe Val Ser	
130 135 140	
ggc gga ccg atg gcg gca gga aga aca agt tac ggg cga aaa atc tcc	480
Gly Gly Pro Met Ala Ala Gly Arg Thr Ser Tyr Gly Arg Lys Ile Ser	
145 150 155 160	
ctt tcc tca gta ttc gaa ggg gta ggc gcc tac caa gca ggg aaa atc	528
Leu Ser Ser Val Phe Glu Gly Val Gly Ala Tyr Gln Ala Gly Lys Ile	
165 170 175	
aac gaa aac gag ctt caa gaa cta gag cag ttc gga tgc cca acg tgc	576
Asn Glu Asn Glu Leu Gln Glu Leu Glu Gln Phe Gly Cys Pro Thr Cys	
180 185 190	
ggg tct tgc tca ggc atg ttt acg gcg aac tca atg aac tgt ctg tca	624
Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys Leu Ser	
195 200 205	
gaa gca ctt ggt ctt gct ttg ccg ggt aat gga acc att ctg gca aca	672
Glu Ala Leu Gly Leu Ala Leu Pro Gly Asn Gly Thr Ile Leu Ala Thr	
210 215 220	

tct cgc gaa cgc aaa gag ttt gtg aga aaa tcg gct gcg caa tta atg	720
Ser Pro Glu Arg Lys Glu Phe Val Arg Lys Ser Ala Ala Gln Leu Met	
225 230 235 240	
gaa acg att cgc aaa gat atc aaa ccg cgt gat att gtt aca gta aaa	753
Glu Thr Ile Arg Lys Asp Ile Lys Pro Arg Asp Ile Val Thr Val Lys	
245 250 255	
gcg att gat aac gcg ttt gca ctc gat atg gcg ctc gga ggt tct aca	816
Ala Ile Asp Asn Ala Phe Ala Leu Asp Met Ala Leu Gly Gly Ser Thr	
260 265 270	
aat acc gtt ctt cat acc ctt gcc ctt gca aac gaa gcc ggc gtt gaa	864
Asn Thr Val Leu His Thr Leu Ala Leu Ala Asn Glu Ala Gly Val Glu	
275 280 285	
tac tct tta gaa cgc att aac gaa gtc gct gag cgc gtg ccg cac ttg	912
Tyr Ser Leu Glu Arg Ile Asn Glu Val Ala Glu Arg Val Pro His Leu	
290 295 300	
gct aag ctg gcg cct gca tcg gat gtg ttt att gaa gat ctt cac gaa	960
Ala Lys Leu Ala Pro Ala Ser Asp Val Phe Ile Glu Asp Leu His Glu	
305 310 315 320	
gcg ggc ggc gtt tca gcg gct ctg aat gag ctt tcg aag aaa gaa gga	1008
Ala Gly Gly Val Ser Ala Ala Leu Asn Glu Leu Ser Lys Lys Glu Gly	
325 330 335	
gcg ctt cat tta gat gcg ctg act gtt aca gga aaa act ctt gga gaa	1056
Ala Leu His Leu Asp Ala Leu Thr Val Thr Gly Lys Thr Leu Gly Glu	
340 345 350	
acc att gcc gga cat gaa gta aag gat tat gac gtc att cac ccg ctg	1104
Thr Ile Ala Gly His Glu Val Lys Asp Tyr Asp Val Ile His Pro Leu	
355 360 365	
gat caa cca ttc act gaa aag gga ggc ctt gct gtt tta ttc ggt aat	1152
Asp Gln Pro Phe Thr Glu Lys Gly Gly Leu Ala Val Leu Phe Gly Asn	
370 375 380	
cta gct ccg gac ggc gct atc att aaa aca ggc ggc gta cag aat ggg	1200
Leu Ala Pro Asp Gly Ala Ile Ile Lys Thr Gly Gly Val Gln Asn Gly	
385 390 395 400	
att aca aga cac gaa ggg ccg gct gtc gta ttc gat tct cag gac gag	1248
Ile Thr Arg His Glu Gly Pro Ala Val Val Phe Asp Ser Gln Asp Glu	
405 410 415	
gcg ctt gac ggc att atc aac cga aaa gta aaa gaa ggc gac gtt gtc	1296
Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val	
420 425 430	
atc atc aga tac gaa ggg cca aaa ggc gga cct ggc atg ccg gaa atg	1344
Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met	
435 440 445	
ctg gcg cca aca tcc caa atc gtt gga atg gga ctc ggg cca aaa gtg	1392
Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val	
450 455 460	

gca ttg att acg gac gga cgt ttt tcc gga gcc tcc cgt ggc ctc tca 1440
 Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
 465 470 475 480

atc ggc cac gta tca cct gag gcc gct gag ggc ggg ccg ctt gcc ttt 1488
 Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe
 485 490 495

gtt gaa aac gga gac cat att atc gtt gat att gaa aaa cgc atc ttg 1536
 Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu
 500 505 510

gat gta caa gtg cca gaa gaa gag tgg gaa aaa cga aaa gcg aac tgg 1584
 Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp
 515 520 525

aaa ggt ttt gaa ccg aaa gtg aaa acc ggc tac ctg gra cgt tat tct 1632
 Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser
 530 535 540

aaa ctt gtg aca agt gcc aac acc ggc ggt att atg aaa atc 1674
 Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile
 545 550 555

<210> 38

<211> 558

<212> PRT

<213> Bacillus subtilis

<400> 38

Met Ala Glu Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala
 1 5 10 15

Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Glu Glu Asp Phe
 20 25 30

Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro
 35 40 45

Gly His Val His Leu Gln Glu Phe Gly Lys Ile Val Lys Glu Ala Ile
 50 55 60

Arg Glu Ala Gly Gly Val Pro Phe Glu Phe Asn Thr Ile Gly Val Asp
 65 70 75 80

Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser
 85 90 95

Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Val Ser Ala His Trp
 100 105 110

Phe Asp Gly Met Val Cys Ile Pro Asn Cys Asp Lys Ile Thr Pro Gly
 115 120 125

Met Leu Met Ala Ala Met Arg Ile Asn Ile Pro Thr Ile Phe Val Ser
 130 135 140

Gly Gly Pro Met Ala Ala Gly Arg Thr Ser Tyr Gly Arg Lys Ile Ser
 145 150 155 160

Leu Ser Ser Val Phe Glu Gly Val Gly Ala Tyr Gln Ala Gly Lys Ile
 165 170 175
 Asn Glu Asn Glu Leu Gln Glu Leu Glu Gln Phe Gly Cys Pro Thr Cys
 180 185 190
 Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys Leu Ser
 195 200 205
 Glu Ala Leu Gly Leu Ala Leu Pro Gly Asn Gly Thr Ile Leu Ala Thr
 210 215 220
 Ser Pro Glu Arg Lys Glu Phe Val Arg Lys Ser Ala Ala Gln Leu Met
 225 230 235 240
 Glu Thr Ile Arg Lys Asp Ile Lys Pro Arg Asp Ile Val Thr Val Lys
 245 250 255
 Ala Ile Asp Asn Ala Phe Ala Leu Asp Met Ala Leu Gly Gly Ser Thr
 260 265 270
 Asn Thr Val Leu His Thr Leu Ala Leu Ala Asn Glu Ala Gly Val Glu
 275 280 285
 Tyr Ser Leu Glu Arg Ile Asn Glu Val Ala Glu Arg Val Pro His Leu
 290 295 300
 Ala Lys Leu Ala Pro Ala Ser Asp Val Phe Ile Glu Asp Leu His Glu
 305 310 315 320
 Ala Gly Gly Val Ser Ala Ala Leu Asn Glu Leu Ser Lys Lys Glu Gly
 325 330 335
 Ala Leu His Leu Asp Ala Leu Thr Val Thr Gly Lys Thr Leu Gly Glu
 340 345 350
 Thr Ile Ala Gly His Glu Val Lys Asp Tyr Asp Val Ile His Pro Leu
 355 360 365
 Asp Gln Pro Phe Thr Glu Lys Gly Gly Leu Ala Val Leu Phe Gly Asn
 370 375 380
 Leu Ala Pro Asp Gly Ala Ile Ile Lys Thr Gly Gly Val Gln Asn Gly
 385 390 395 400
 Ile Thr Arg His Glu Gly Pro Ala Val Val Phe Asp Ser Gln Asp Glu
 405 410 415
 Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val
 420 425 430
 Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met
 435 440 445
 Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val
 450 455 460
 Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
 465 470 475 480
 Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe

	485		490		495
Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu					
	500		505		510
Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp					
	515		520		525
Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser					
	530		535		540
Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile					
	545		550		555

<110> 39
 <111> 194
 <112> DNA
 <113> Artificial Sequence

<110>
 <113> Description of Artificial Sequence:promoter
 sequence

<110>
 <111> -35_signal
 <112> (136)..(141)

<110>
 <111> -10_signal
 <112> (159)..(164)

<400> 39
 gctattgacg acagctatgg ttcactgtcc accaaccaaa actgtgctca gtaccgccaa 60
 tattttctccc ttgaggggta caaagagggtg tcctagaag agatccacgc tgtgtaaaaa 120
 ttttacaaaa aggtattgac tttccctaca ggggtgtgtaa taatttaatt acaggcgggg 180
 gcaaccccgcc ctgt 194

<110> 40
 <111> 163
 <112> DNA
 <113> Artificial Sequence

<110>
 <113> Description of Artificial Sequence:promoter
 sequence

<110>
 <111> -35_signal
 <112> (113)..(118)

<110>
 <111> -10_signal
 <112> (136)..(141)

<400> 40
 gcttacctag cttccaagaa agatatccta acagcacaag agcggaaaga tgttttggtc 60

tacatccaga acaacctctg ctaaaattcc tgaaaaattt tgcaaaaagt tgttgacttt 120
atctacaagg tgtggtataa taatcttaac aacagcagga cgc 163

<210> 41
<211> 127
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
sequence

<210>
<221> -35_signal
<222> (34)..(39)

<210>
<221> -10_signal
<222> (53)..(63)

<210>
<221> -35_signal
<222> (75)..(80)

<210>
<221> -10_signal
<222> (93)..(103)

<400> 41
gaggaatcat agaattttgt caaaataatt ttattgacaa cgtcttatta acgttgatat 60
aatttaaatt ttatttgaca aaaatgggct cgtgttgtac aataaatgta gtgaggtgga 120
tgcaatg 127

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 42
taaacatgag gaggagaaaa catg 24

<210> 43
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 43

attcgagaaa tggagagaat ataatatg

28

<210> 44

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 44

agaaaggagg tga

13

<210> 45

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 45

ttaagaaagg aggtgannnn atg

23

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 46

ttagaaagga ggtgannnnn atg

23

<210> 47

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 47

agaaaggagg tgannnnnnn atg

23

<210> 48

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 48
agaaaggagg tgannnnnna tg 22

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 49
ccctctagaa ggaggagaaa acatg 25

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 50
ccctctagag gaggagaaaa catg 24

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 51
ttagaaagga ggatttaa atg 23

<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 52
ttagaaagga ggtttaatta atg 23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 53

ttagaaagga ggtgatttaa atg

23

<210> 54

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 54

ttagaaagga ggtgttttaa atg

23

<210> 55

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 55

attcgagaaa ggaggtgaat ataatatg

28

<210> 56

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 56

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27

<210> 57

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 57

attcgtagaa aggaggtgaa ttaatatg

28

<210> 58

<211> 3291

<212> DNA

<213> Bacillus subtilis

<400> 58

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ggcggggctg tgcttccgat ttacgataag ctatacaatt cagggttggt acatatacctt 180
ccccgtcacg aacaaggagc aattcatgca ggggagggat acgcaagggt ctcgggaaaa 240
ccgggtgtcg tcattgccac gtcagggccg ggagcgacaa accttggtac aggccttgct 300
gatgccatga ttgattcatt gccgttagtc gtctttacag ggcaggtagc aacctctgta 360
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cacagctacc aggttcgcca gccggaagat ctgcgcgcga tcattaaaga agcgttccat 480
attgcaacaa ctggaagacc cggacctgta ttgattgata ttccgaaaga tgtagcaaca 540
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<210> 59

<211> 2363

<212> DNA

<213> Bacillus subtilis

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<221> CDS

<222> (242)..(1072)

<220>

<221> CDS

<222> (1077)..(1934)

<220>

<221> CDS

<222> (1939)..(2319)

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cctattatta aaatagatag acattgcagc agtctgcctt gatccaaaaa aggactggga 120

cagagggatg aaactcgccg aacttttagaa agtgaagaat ccttctcggt gtaacggaag 180

gttttttggc ttgcagaaga aaacggcaga tcctctcctc taaacatgag gaggagaaaa 240

c atg aaa aca aaa ctg gat ttt cta aaa atg aag gag tct gaa gaa ccg 289

Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro

1

5

10

15

att gtc atg ctg acc gct tat gat tat ccg gca gct aaa ctt gct gaa 337

Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu

20

25

30

caa gcg gga gtt gac atg att tta gtc ggt gat tca ctt gga atg gtc 385

Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val

35

40

45

gtc ctc ggc ctt gat tca act gtc ggt gtg aca gtt gcg gac atg atc 413

Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile

50

55

60

cat cat aca aaa gcc gtt aaa agg ggt gcg ccg aat acc ttt att gtg 481

His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val

65

70

75

80

aca gat atg ccg ttt atg tct tat cac ctg tct aag gaa gat acg ctg 529

Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu

85

90

95

aaa aat gca gcg gct atc gtt cag gaa agc gga gct gac gca ctg aag 577

Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys

100

105

110

ctt gag ggc gga gaa ggc gtg ttt gaa tcc att cgc gca ttg acg ctt 625

Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu

115

120

125

gga ggc att cca gta gtc agt cac tta ggt ttg aca ccg cag tca gtc 673

Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val

130

135

140

ggc gta ctg ggc ggc tat aaa gta cag ggc aaa gac gaa caa agc gcc 721

Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala

145

150

155

160

aaa aaa tta ata gaa gac agt ata aaa tgc gaa gaa gca gga gct atg 769

Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met

165

170

175

atg ctt gtg ctg gaa tgt gtg ccg gca gaa ctc aca gcc aaa att gcc 817

Met Leu Val Leu Glu Cys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala

180

185

190

gag acg cta agc ata ccg gtc att gga atc ggg gct ggt gtg aaa gcg 865

Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala	
195 200 205	
gac gga caa gtt ctc gtt tat cat gat att atc ggc cac ggt gtt gag	913
Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Glu	
210 215 220	
aga aca cct aaa ttt gta aag caa tat acg cgc att gat gaa acc atc	951
Arg Thr Pro Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile	
225 230 235 240	
gaa aca gca atc agc gga tat gtt cag gat gta aga cat cgt gct ttc	1009
Glu Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Phe	
245 250 255	
cct gaa caa aag cat tcc ttt caa atg aac cag aca gtg ctt gac ggc	1057
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly	
260 265 270	
ttg tac ggg gga aaa taag atg aga cag att act gat att tca cag ctg	1105
Leu Tyr Gly Gly Lys Met Arg Gln Ile Thr Asp Ile Ser Gln Leu	
275 280 285	
aaa gaa gcc ata aaa caa tac cat tca gag ggc aag tca atc gga ttt	1154
Lys Glu Ala Ile Lys Gln Tyr His Ser Glu Gly Lys Ser Ile Gly Phe	
290 295 300	
gtt ccg acg atg ggg ttt ctg cat gag ggg cat tta acc tta gca gac	1202
Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu Thr Leu Ala Asp	
305 310 315	
aaa gca aga caa gaa aac gac gcc gtt att atg agt att ttt gtg aat	1250
Lys Ala Arg Gln Glu Asn Asp Ala Val Ile Met Ser Ile Phe Val Asn	
320 325 330 335	
cct gca caa ttc ggc cct aat gaa gat ttt gaa gca tat ccg cgc gat	1298
Pro Ala Gln Phe Gly Pro Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp	
340 345 350	
att gag cgg gat gca gct ctt gca gaa aac gcc gga gtc gat att ctt	1345
Ile Glu Arg Asp Ala Ala Leu Ala Glu Asn Ala Gly Val Asp Ile Leu	
355 360 365	
ttt acg cca gat gct cat gat atg tat ccc ggt gaa aag aat gtc acg	1394
Phe Thr Pro Asp Ala His Asp Met Tyr Pro Gly Glu Lys Asn Val Thr	
370 375 380	
att cat gta gaa aga cgc aca gac gtg tta tgc ggg cgc tca aga gaa	1442
Ile His Val Glu Arg Arg Thr Asp Val Leu Cys Gly Arg Ser Arg Glu	
385 390 395	
gga cat ttt gac ggg gtc gcg atc gta ctg acg aag ctt ttc aat cta	1490
Gly His Phe Asp Gly Val Ala Ile Val Leu Thr Lys Leu Phe Asn Leu	
400 405 410 415	
gtc aag ccg act cgt gcc tat ttc ggt tta aaa gat ggc cag cag gta	1538
Val Lys Pro Thr Arg Ala Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val	
420 425 430	
gct gtt gtt gat ggg tta atc agc gac ttc ttc atg gat att gaa ttg	1586
Ala Val Val Asp Gly Leu Ile Ser Asp Phe Phe Met Asp Ile Glu Leu	

435										440					445					
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Val	Pro	Val	Asp	Thr	Val	Arg	Glu	Glu	Asp	Gly	Leu	Ala	Lys	Ser	Ser					
450					455					460										
cgc	aat	gta	tac	tta	aca	gct	gag	gaa	aga	aaa	gaa	gcg	cct	aag	ctg	1682				
Arg	Asn	Val	Tyr	Leu	Thr	Ala	Glu	Glu	Arg	Lys	Glu	Ala	Pro	Lys	Leu					
465					470					475										
tat	cgg	gcc	ctt	caa	aca	agt	gcg	gaa	ctt	gtc	caa	gcc	ggc	gaa	aga	1730				
Tyr	Arg	Ala	Leu	Gln	Thr	Ser	Ala	Glu	Leu	Val	Gln	Ala	Gly	Glu	Arg					
480					485					490					495					
gat	cct	gaa	gcg	gtg	ata	aaa	gct	gca	aaa	gat	atc	att	gaa	acg	act	1778				
Asp	Pro	Glu	Ala	Val	Ile	Lys	Ala	Ala	Lys	Asp	Ile	Ile	Glu	Thr	Thr					
500					505					510										
agc	gga	acc	ata	gac	tat	gta	gag	ctt	tat	tcc	tat	cgc	gaa	ctc	gag	1826				
Ser	Gly	Thr	Ile	Asp	Tyr	Val	Glu	Leu	Tyr	Ser	Tyr	Pro	Glu	Leu	Glu					
515					520					525										
cct	gtg	aat	gaa	att	gct	gga	aag	atg	att	ctc	gct	gtt	gca	gtt	gct	1874				
Pro	Val	Asn	Glu	Ile	Ala	Gly	Lys	Met	Ile	Leu	Ala	Val	Ala	Val	Ala					
530					535					540										
ttt	tca	aaa	gcg	cgt	tta	ata	gat	aat	atc	att	att	gat	att	cga	gaa	1922				
Phe	Ser	Lys	Ala	Arg	Leu	Ile	Asp	Asn	Ile	Ile	Ile	Asp	Ile	Arg	Glu					
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Met	Glu	Arg	Ile		Met	Tyr	Arg	Thr	Met	Met	Ser	Gly	Lys	Leu	His					
560					565					570										
agg	gca	act	gtt	acg	gaa	gca	aac	ctg	aac	tat	gtg	gga	agc	att	aca	2019				
Arg	Ala	Thr	Val	Thr	Glu	Ala	Asn	Leu	Asn	Tyr	Val	Gly	Ser	Ile	Thr					
575					580					585					590					
att	gat	gaa	gat	ctc	att	gat	gct	gtg	gga	atg	ctt	cct	aat	gaa	aaa	2067				
Ile	Asp	Glu	Asp	Leu	Ile	Asp	Ala	Val	Gly	Met	Leu	Pro	Asn	Glu	Lys					
595					600					605										
gta	caa	att	gtg	aat	aat	aat	aat	gga	gca	cgt	ctt	gaa	acg	tat	att	2115				
Val	Gln	Ile	Val	Asn	Asn	Asn	Asn	Gly	Ala	Arg	Leu	Glu	Thr	Tyr	Ile					
610					615					620										
att	cct	ggc	aaa	cgg	gga	agc	ggc	gtc	ata	tgc	tta	aac	ggc	gca	gcc	2163				
Ile	Pro	Gly	Lys	Arg	Gly	Ser	Gly	Val	Ile	Cys	Leu	Asn	Gly	Ala	Ala					
625					630					635										
gca	cgc	ctt	gtg	cag	gaa	gga	gat	aag	gtc	att	att	att	tcc	tac	aaa	2211				
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640					645					650										
atg	atg	tct	gat	caa	gaa	gag	gca	agc	cat	gag	cgc	aaa	gtg	gct	gtt	2259				
Met	Met	Ser	Asp	Gln	Glu	Ala	Ala	Ser	His	Glu	Pro	Lys	Val	Ala	Val					
655					660					665					670					
ctg	aat	gat	caa	aac	aaa	att	gaa	caa	atg	ctg	ggg	aac	gaa	cca	gcc	2307				
Leu	Asn	Asp	Gln	Asn	Lys	Ile	Glu	Gln	Met	Leu	Gly	Asn	Glu	Pro	Ala					
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 Arg Thr Ile Leu
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<210> 60

<211> 293

<212> PRT

<213> Bacillus subtilis

<400> 60

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 20 25 30

Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala Glu Arg Asn Lys
 35 40 45

His Val Asn Val Phe Leu Lys His Pro His Ser Ala Lys Ile Pro Phe
 50 55 60

Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala
 65 70 75 80

Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp Arg Pro Lys Val
 85 90 95

Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys
 100 105 110

Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val
 115 120 125

Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser
 130 135 140

Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Glu Glu Gly
 145 150 155 160

Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
 165 170 175

Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg
 180 185 190

Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu
 195 200 205

Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg
 210 215 220

Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
 225 230 235 240

Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
 245 250 255

Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg

Ile Trp Glu Ser Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro

245

250

255

Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys
 250 265 270

Val Glu Glu Val Leu Val Arg Arg Val
 275 280

<110> 62

<111> 1092

<112> DNA

<113> Bacillus subtilis

<120>

<121> CDS

<122> (1)..(1039)

<400> 62

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aaa cca gac cca aat cag ctt tcc gga aga gtg ttt aca gac cac 96
 Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
 20 25 30

atg ttt gta atg gac tat gcc gca gat aaa ggt tgg tac gat cca aga 144
 Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
 35 40 45

atc att cct tat caa ccc tta tca atg gat cca act gca atg gtc tat 192
 Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
 50 55 60

cac tac ggc caa acc gtg ttt gaa ggg tta aag gct tac gtg tca gag 240
 His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
 65 70 75 80

gat gac cat gtt ctg ctt ttc aga ccg gaa aaa aat atg gaa cgc ctg 288
 Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
 85 90 95

aat caa tca aac gac cgc ctc tgc atc ccg caa att gat gaa gaa cag 336
 Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
 100 105 110

gtt ctt gaa ggc tta aag cag ctt gtc gca att gat aaa gac tgg att 384
 Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
 115 120 125

cca aat gcg gag ggc acg tcc ctt tac atc cgt ccg ttc atc atc gca 432
 Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
 130 135 140

acc gag cct ttc ctt ggt gtt gcg gca tct cat acg tat aag ctc ttg 480
 Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
 145 150 155 160

atc att ctt tct ccg gtc ggc tct tat tac aaa gaa ggc att aag ccg 528
 Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro

	165	170	175	
gtc aaa atc gct gtt gaa agt gaa ttt gtc cgt gcg gta aaa ggc gga				576
Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly				
	130	185	190	
aca gga aat gcc aaa acc gca gga aac tat gct tca agc tta aaa gcg				624
Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala				
	195	200	205	
cag cag gta gcc gaa gag aaa gga ttt tct caa gta ctc tgg ctg gac				672
Gln Gln Val Ala Glu Glu Lys Gly Phe Ser Gln Val Leu Trp Leu Asp				
	210	215	220	
ggc att gag aag aaa tac atc gaa gaa gtc gga agc atg aac atc ttc				720
Gly Ile Glu Lys Lys Tyr Ile Glu Glu Val Gly Ser Met Asn Ile Phe				
	225	230	235	240
ttc aaa atc aac ggt gaa atc gta aca ccg atg ctg aac ggg agc atc				768
Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile				
	245	250	255	
ctg gaa ggc att acg cgc aat tca gtc atc gcc ttg ctt aag cat tgg				816
Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp				
	260	265	270	
ggc ctt caa gtt tca gaa cga aaa att gcg atc gat gag gtc atc caa				864
Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln				
	275	280	285	
gcc cat aaa gac ggc atc ctg gaa gaa gcc ttc gga aca ggt aca gca				912
Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala				
	290	295	300	
gct gtt att tcc cca gtc ggc gag ctg atc tgg cag gat gaa aca ctt				960
Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu				
	305	310	315	320
tcg atc aac aac ggt gaa aca gga gaa atc gca aaa aaa cta tat gac				1008
Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp				
	325	330	335	
acg att aca ggc att caa aaa ggc gct gtc gca gac gaa ttc gga tgg				1056
Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp				
	340	345	350	
acg acc gaa gtc gca gcg ctg act gaa agc aag taa				1092
Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys				
	355	360		

<210> 63

<211> 363

<212> PRT

<213> Bacillus subtilis

<400> 63

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Lys	Pro	Asp	Pro	Asn	Gln	Leu	Ser	Phe	Gly	Arg	Val	Phe	Thr	Asp	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

			20					25					30			
Met	Phe	Val	Met	Asp	Tyr	Ala	Ala	Asp	Lys	Gly	Trp	Tyr	Asp	Pro	Arg	
		35					40						45			
Ile	Ile	Pro	Tyr	Gln	Pro	Leu	Ser	Met	Asp	Pro	Thr	Ala	Met	Val	Tyr	
	50					55					60					
His	Tyr	Gly	Gln	Thr	Val	Phe	Glu	Gly	Leu	Lys	Ala	Tyr	Val	Ser	Glu	
65					70					75					80	
Asp	Asp	His	Val	Leu	Leu	Phe	Arg	Pro	Glu	Lys	Asn	Met	Glu	Arg	Leu	
				85					90					95		
Asn	Gln	Ser	Asn	Asp	Arg	Leu	Cys	Ile	Pro	Gln	Ile	Asp	Glu	Glu	Gln	
			100					105					110			
Val	Leu	Glu	Gly	Leu	Lys	Gln	Leu	Val	Ala	Ile	Asp	Lys	Asp	Trp	Ile	
		115					120						125			
Pro	Asn	Ala	Glu	Gly	Thr	Ser	Leu	Tyr	Ile	Arg	Pro	Phe	Ile	Ile	Ala	
	130					135					140					
Thr	Glu	Pro	Phe	Leu	Gly	Val	Ala	Ala	Ser	His	Thr	Tyr	Lys	Leu	Leu	
145					150					155					160	
Ile	Ile	Leu	Ser	Pro	Val	Gly	Ser	Tyr	Tyr	Lys	Glu	Gly	Ile	Lys	Pro	
				165					170					175		
Val	Lys	Ile	Ala	Val	Glu	Ser	Glu	Phe	Val	Arg	Ala	Val	Lys	Gly	Gly	
			180					185					190			
Thr	Gly	Asn	Ala	Lys	Thr	Ala	Gly	Asn	Tyr	Ala	Ser	Ser	Leu	Lys	Ala	
		195					200					205				
Gln	Gln	Val	Ala	Glu	Glu	Lys	Gly	Phe	Ser	Gln	Val	Leu	Trp	Leu	Asp	
		210				215					220					
Gly	Ile	Glu	Lys	Lys	Tyr	Ile	Glu	Glu	Val	Gly	Ser	Met	Asn	Ile	Phe	
225					230					235					240	
Phe	Lys	Ile	Asn	Gly	Glu	Ile	Val	Thr	Pro	Met	Leu	Asn	Gly	Ser	Ile	
				245					250					255		
Leu	Glu	Gly	Ile	Thr	Arg	Asn	Ser	Val	Ile	Ala	Leu	Leu	Lys	His	Trp	
			260					265					270			
Gly	Leu	Gln	Val	Ser	Glu	Arg	Lys	Ile	Ala	Ile	Asp	Glu	Val	Ile	Gln	
		275					280					285				
Ala	His	Lys	Asp	Gly	Ile	Leu	Glu	Glu	Ala	Phe	Gly	Thr	Gly	Thr	Ala	
						295					300					
Ala	Val	Ile	Ser	Pro	Val	Gly	Glu	Leu	Ile	Trp	Gln	Asp	Glu	Thr	Leu	
305					310					315					320	
Ser	Ile	Asn	Asn	Gly	Glu	Thr	Gly	Glu	Ile	Ala	Lys	Lys	Leu	Tyr	Asp	
				325					330					335		
Thr	Ile	Thr	Gly	Ile	Gln	Lys	Gly	Ala	Val	Ala	Asp	Glu	Phe	Gly	Trp	
			340					345					350			

Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys
 355 360

<210> 64
 <211> 1071
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1068)

<400> 64
 ttg aat aag ctt att gaa cga gaa aaa act gta tat tat aag gaa aag 48
 Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys
 1 5 10 15
 ccc gac ccg tct tcc ttg ggg ttt gga caa tat ttt aca gat tat atg 96
 Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met
 20 25 30
 ttt gtg atg gac tac gaa gag ggg att gga tgg cat cat ccg aga att 144
 Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile
 35 40 45
 gcg ccg tac gca ccg ctt acg ctt gat ccg tct tca tct gtt ttt cat 192
 Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His
 50 55 60
 tac ggc cag gct gtt ttt gaa gga tta aaa gca tac aga aca gac gac 240
 Tyr Gly Gln Ala Val Phe Glu Gly Leu Lys Ala Tyr Arg Thr Asp Asp
 65 70 75 80
 ggc agg gtg ctg ctg ttc cgt ccg gat caa aat atc aaa ccg ctg aac 288
 Gly Arg Val Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn
 85 90 95
 aga tcg tgt gag cgc atg agc atg ccc cct tta gac gaa gag ctg gtg 336
 Arg Ser Cys Glu Arg Met Ser Met Pro Pro Leu Asp Glu Glu Leu Val
 100 105 110
 ctt gag gca ttg acg caa tta gtt gag ctg gag aaa gat tgg gtt cca 384
 Leu Glu Ala Leu Thr Gln Leu Val Glu Leu Glu Lys Asp Trp Val Pro
 115 120 125
 aag gaa aaa gga acg tca ctg tat att cgt cct ttt gtc att gcc aca 432
 Lys Glu Lys Gly Thr Ser Leu Tyr Ile Arg Pro Phe Val Ile Ala Thr
 130 135 140
 gaa ccg agt ctc ggt gtg aag gca tcc agg agc tat aca ttt atg atc 480
 Glu Pro Ser Leu Gly Val Lys Ala Ser Arg Ser Tyr Thr Phe Met Ile
 145 150 155 160
 gtg ctt tcc cct gtc ggc tcc tat tat ggc gac gat cag ctg aag ccg 528
 Val Leu Ser Pro Val Gly Ser Tyr Tyr Gly Asp Asp Gln Leu Lys Pro
 165 170 175
 gtt aga atc tat gtc gaa gat gag tat gtg agg ggc gtc aac gga gga 576
 Val Arg Ile Tyr Val Glu Asp Glu Tyr Val Arg Ala Val Asn Gly Gly

	130	185	190	
gtc ggg ttt gca aaa acg gct gga aac tat gcc gcc agt ctt cag gca				624
Val Gly Phe Ala Lys Thr Ala Gly Asn Tyr Ala Ala Ser Leu Gln Ala				
	195	200	205	
cag cgg aaa gcg aat gaa ctg ggc tat gac cag gta ctg tgg ctg gac				672
Gln Arg Lys Ala Asn Glu Leu Gly Tyr Asp Gln Val Leu Trp Leu Asp				
	210	215	220	
gcc atc gaa aag aaa tat gtg gaa gaa gta ggg agc atg aac atc ttt				720
Ala Ile Glu Lys Lys Tyr Val Glu Glu Val Gly Ser Met Asn Ile Phe				
	225	230	235	240
ttc gtc ata aac ggg gaa gct gtc aca cct gct tta agc gga agc att				768
Phe Val Ile Asn Gly Glu Ala Val Thr Pro Ala Leu Ser Gly Ser Ile				
	245	250	255	
tta agc ggg gtt aca cgt gcg tct gcg att gaa ttg att cga agc tgg				816
Leu Ser Gly Val Thr Arg Ala Ser Ala Ile Glu Leu Ile Arg Ser Trp				
	260	265	270	
ggc att ccg gtt cgt gaa gag aga ata tcg att gat gag gtg tat gcg				864
Gly Ile Pro Val Arg Glu Glu Arg Ile Ser Ile Asp Glu Val Tyr Ala				
	275	280	285	
gcc tct gca cgc gga gaa ttg aca gag gtc ttt ggc aca ggc acg gca				912
Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala				
	290	295	300	
gca gtc gtt acg cct gtc ggt gaa ctg aac atc cat gga aaa acg gtg				960
Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val				
	305	310	315	320
att gta ggc gac ggg caa atc ggg gac ctg tcg aaa aag ctg tat gaa				1008
Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu				
	325	330	335	
acg ata aca gat att cag ctt ggc aag gta aaa ggc ccg ttt aac tgg				1056
Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp				
	340	345	350	
aca gtg gaa gtg tga				1071
Thr Val Glu Val				
	355			
<210> 65				
<211> 356				
<212> PRT				
<213> Bacillus subtilis				
<400> 65				
Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys				
1 5 10 15				
Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met				
20 25 30				
Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile				
35 40 45				

Thr Val Glu Val
355

<210> 66
 <211> 1428
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1425)

<400> 66
 atg tta aac ggc caa aaa gaa tat cgc gtg gaa aaa gac ttc ctt ggg 48
 Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
 1 5 10 15

gaa aaa caa att gaa gca gat gtt tat tac gga att cag acg ctc cgt 96
 Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
 20 25 30

gct tct gaa aat ttt ccg atc aca gga tac aaa atc cat gag gaa atg 144
 Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
 35 40 45

att aac gca ctg gcg att gtg aaa aaa gct gcg gct ctt gcc aac atg 192
 Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
 50 55 60

gac gtg aaa cgg ctg tat gaa gga att ggc caa gct atc gta caa gcc 240
 Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
 65 70 75 80

gct gac gag att ctg gaa ggc aag tgg cac gat cag ttt atc gtc gat 288
 Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp
 85 90 95

ccg att cag ggc ggt gcc gga act tct atg aac atg aac gcg aat gag 336
 Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu
 100 105 110

gtt atc gga aac cgg gcg ctt gaa atc atg gga cat aaa aag gga gat 384
 Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp
 115 120 125

tat atc cat tta agt cca aac aca cat gtg aac atg tca cag tct cag 432
 Tyr Ile His Leu Ser Pro Asn Thr His Val Asn Met Ser Gln Ser Gln
 130 135 140

aac gat gtg ttc ccg act gct atc cat att tcc aca ttg aag ctc tta 480
 Asn Asp Val Phe Pro Thr Ala Ile His Ile Ser Thr Leu Lys Leu Leu
 145 150 155 160

gaa aaa ctg ctg aaa aca atg gaa gat atg cat agt gtg ttt aaa caa 528
 Glu Lys Leu Leu Lys Thr Met Glu Asp Met His Ser Val Phe Lys Gln
 165 170 175

aaa gca cag gag ttt cac tct gtt att aaa atg ggc cgg aca cac ctt 576
 Lys Ala Gln Glu Phe His Ser Val Ile Lys Met Gly Arg Thr His Leu
 180 185 190

caa gat gcg gtt ccg atc cgt ctt ggc cag gaa ttc gaa gct tac agc 624
 Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser

195	200	205	
cgt gtt ctc gag cgt gat atc aaa cga atc aag caa tcg cgc cag cac Arg Val Leu Glu Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His 210 215 220			672
ctg tat gaa gtc aac atg ggc gca act gct gtt ggt aca ggg ctg aac Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn 225 230 235 240			720
gct gat cct gaa tat atc aaa cag gta gta aag cac ctt gct gat att Ala Asp Pro Glu Tyr Ile Lys Gln Val Val Lys His Leu Ala Asp Ile 245 250 255			768
agc ggg ctt cct ctt gtc ggc gct gat cat ctt gtt gat ggc aca caa Ser Gly Leu Pro Leu Val Gly Ala Asp His Leu Val Asp Ala Thr Gln 260 265 270			816
aat aca gat gcc tat aca gag gta tca gct tca tta aaa gtc tgc atg Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ser Leu Lys Val Cys Met 275 280 285			864
atg aac atg tcg aag atc gca aac gac ctg cgc tta atg ggc tcg gga Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala Ser Gly 290 295 300			912
ccg cgc gcc gga ctt gcg gaa att tct ctg cct gca cgt cag ccg ggt Pro Arg Ala Gly Leu Ala Glu Ile Ser Leu Pro Ala Arg Gln Pro Gly 305 310 315 320			960
tca tct att atg ccg ggg aaa gtc aat ccg gtt atg gcg gag ctg atc Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Leu Ile 325 330 335			1008
aac caa att gcg ttc cag gtt atc gga aat gac aat aca atc tgc ctt Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp Asn Thr Ile Cys Leu 340 345 350			1056
gct tca gaa gcc ggc cag ctt gag ttg aac gtc atg gag ccc gtg ctt Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu 355 360 365			1104
gtc ttt aat ttg ctt caa tcc atc agc atc atg aac aac ggc ttc cgt Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg 370 375 380			1152
tcg ttc act gac aac tgc tta aaa ggc att gaa gcc aac gaa aag cgt Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu Lys Arg 385 390 395 400			1200
atg aag caa tac gta gaa aaa agc gca ggc gtg atc aca gct gtc aat Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn 405 410 415			1248
ccg cat ctt ggg tat gaa gcg gca gct aga att gcc agg gaa gca att Pro His Leu Gly Tyr Glu Ala Ala Ala Arg Ile Ala Arg Glu Ala Ile 420 425 430			1296
atg aca ggg caa tct gtc cgg gat ctt tgt ctg cag cat gat gtg ctg Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu 435 440 445			1344

act gaa gaa gaa ttg gat att att tta aac cca tat gag atg acc aaa 1392
 Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
 450 455 460

cca ggt atc gca ggg aaa gaa cta tta gaa aaa taa 1428
 Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
 465 470 475

<210> 57

<211> 475

<212> PRF

<213> Bacillus subtilis

<400> 57

Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
 1 5 10 15

Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
 20 25 30

Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
 35 40 45

Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
 50 55 60

Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
 65 70 75 80

Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp
 85 90 95

Pro Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu
 100 105 110

Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp
 115 120 125

Tyr Ile His Leu Ser Pro Asn Thr His Val Asn Met Ser Gln Ser Gln
 130 135 140

Asn Asp Val Phe Pro Thr Ala Ile His Ile Ser Thr Leu Lys Leu Leu
 145 150 155 160

Glu Lys Leu Leu Lys Thr Met Glu Asp Met His Ser Val Phe Lys Gln
 165 170 175

Lys Ala Gln Glu Phe His Ser Val Ile Lys Met Gly Arg Thr His Leu
 180 185 190

Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser
 195 200 205

Arg Val Leu Glu Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His
 210 215 220

Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn
 225 230 235 240

Ala Asp Pro Glu Tyr Ile Lys Gln Val Val Lys His Leu Ala Asp Ile
 245 250 255
 Ser Gly Leu Pro Leu Val Gly Ala Asp His Leu Val Asp Ala Thr Gln
 260 265 270
 Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ser Leu Lys Val Cys Met
 275 280 285
 Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala Ser Gly
 290 295 300
 Pro Arg Ala Gly Leu Ala Glu Ile Ser Leu Pro Ala Arg Gln Pro Gly
 305 310 315 320
 Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Leu Ile
 325 330 335
 Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp Asn Thr Ile Cys Leu
 340 345 350
 Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu
 355 360 365
 Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg
 370 375 380
 Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu Lys Arg
 385 390 395 400
 Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn
 405 410 415
 Pro His Leu Gly Tyr Glu Ala Ala Ala Arg Ile Ala Arg Glu Ala Ile
 420 425 430
 Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu
 435 440 445
 Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
 450 455 460
 Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
 465 470 475

<210> 68

<211> 763

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(765)

<400> 68

atg aaa cga gaa agc aac att caa gtg ctc agc cgt ggt caa aaa gat 48
 Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
 1 5 10 15

cag cct gtg agc cag att tat caa gta tca aca atg act tct cta tta 96

Gln	Pro	Val	Ser	Gln	Ile	Tyr	Gln	Val	Ser	Thr	Met	Thr	Ser	Leu	Leu	
			20					25					30			
gac	gga	gta	tat	gac	gga	gat	ttt	gaa	ctg	tca	gag	att	cgc	aaa	tat	144
Asp	Gly	Val	Tyr	Asp	Gly	Asp	Phe	Glu	Leu	Ser	Glu	Ile	Pro	Lys	Tyr	
		35					40					45				
gga	gac	ttc	ggc	atc	gga	acc	ttt	aac	aag	ctt	gac	gga	gag	ctg	att	192
Gly	Asp	Phe	Gly	Ile	Gly	Thr	Phe	Asn	Lys	Leu	Asp	Gly	Glu	Leu	Ile	
		50				55					60					
ggg	ttt	gac	ggc	gaa	ttt	tac	cgt	ctt	cgc	tca	gac	gga	acc	gcg	aca	240
Gly	Phe	Asp	Gly	Glu	Phe	Tyr	Arg	Leu	Arg	Ser	Asp	Gly	Thr	Ala	Thr	
	65				70				75						80	
cgc	gtc	caa	aat	gga	gac	cgt	tca	cgc	ttc	tgt	tca	ttt	acg	ttc	ttt	288
Pro	Val	Gln	Asn	Gly	Asp	Arg	Ser	Pro	Phe	Cys	Ser	Phe	Thr	Phe	Phe	
			85					90						95		
aca	cgc	gac	atg	acg	cac	aaa	att	gat	gcg	aaa	atg	aca	cgc	gaa	gac	336
Thr	Pro	Asp	Met	Thr	His	Lys	Ile	Asp	Ala	Lys	Met	Thr	Arg	Glu	Asp	
			100					105					110			
ttt	gaa	aaa	gag	atc	aac	agc	atg	ctg	cca	agc	aga	aac	tta	ttt	tat	384
Phe	Glu	Lys	Glu	Ile	Asn	Ser	Met	Leu	Pro	Ser	Arg	Asn	Leu	Phe	Tyr	
		115					120					125				
gca	att	cgc	att	gac	gga	ttg	ttt	aaa	aag	gtg	cag	aca	aga	aca	gta	432
Ala	Ile	Arg	Ile	Asp	Gly	Leu	Phe	Lys	Lys	Val	Gln	Thr	Arg	Thr	Val	
		130				135					140					
gaa	ctt	caa	gaa	aaa	cct	tac	gtg	cca	atg	gtt	gaa	gcg	gtc	aaa	aca	480
Glu	Leu	Gln	Glu	Lys	Pro	Tyr	Val	Pro	Met	Val	Glu	Ala	Val	Lys	Thr	
	145				150				155						160	
cag	cgc	att	ttc	aac	ttc	gac	aac	gtg	aga	gga	acg	att	gta	ggc	ttc	528
Gln	Pro	Ile	Phe	Asn	Phe	Asp	Asn	Val	Arg	Gly	Thr	Ile	Val	Gly	Phe	
				165				170						175		
ttg	aca	cca	gct	tat	gca	aac	gga	atc	gcc	gtt	tct	ggc	tat	cac	ctg	576
Leu	Thr	Pro	Ala	Tyr	Ala	Asn	Gly	Ile	Ala	Val	Ser	Gly	Tyr	His	Leu	
			180				185						190			
cac	ttc	att	gac	gaa	gga	cgc	aat	tca	ggc	gga	cac	gtt	ttt	gac	tat	624
His	Phe	Ile	Asp	Glu	Gly	Arg	Asn	Ser	Gly	Gly	His	Val	Phe	Asp	Tyr	
		195					200					205				
gtg	ctt	gag	gat	tgc	acg	gtt	acg	att	tct	caa	aaa	atg	aac	atg	aat	672
Val	Leu	Glu	Asp	Cys	Thr	Val	Thr	Ile	Ser	Gln	Lys	Met	Asn	Met	Asn	
	210					215					220					
ctc	aga	ctt	cgc	aac	aca	gcg	gat	ttc	ttt	aat	gcg	aat	ctg	gat	aac	720
Leu	Arg	Leu	Pro	Asn	Thr	Ala	Asp	Phe	Phe	Asn	Ala	Asn	Leu	Asp	Asn	
	225				230					235					240	
cct	gat	ttt	gcg	aaa	gat	atc	gaa	aca	act	gaa	gga	agc	cct	gaa	taa	768
Pro	Asp	Phe	Ala	Lys	Asp	Ile	Glu	Thr	Thr	Glu	Gly	Ser	Pro	Glu		
				245				250						255		

<211> 255

<212> PRT

<213> Bacillus subtilis

<400> 69

Met	Lys	Arg	Glu	Ser	Asn	Ile	Gln	Val	Leu	Ser	Arg	Gly	Gln	Lys	Asp
1				5					10					15	

Gln	Pro	Val	Ser	Gln	Ile	Tyr	Gln	Val	Ser	Thr	Met	Thr	Ser	Leu	Leu
			20					25					30		

Asp	Gly	Val	Tyr	Asp	Gly	Asp	Phe	Glu	Leu	Ser	Glu	Ile	Pro	Lys	Tyr
		35					40					45			

Gly	Asp	Phe	Gly	Ile	Gly	Thr	Phe	Asn	Lys	Leu	Asp	Gly	Glu	Leu	Ile
	50					55					60				

Gly	Phe	Asp	Gly	Glu	Phe	Tyr	Arg	Leu	Arg	Ser	Asp	Gly	Thr	Ala	Thr
65					70					75					80

Pro	Val	Gln	Asn	Gly	Asp	Arg	Ser	Pro	Phe	Cys	Ser	Phe	Thr	Phe	Phe
				85					90					95	

Thr	Pro	Asp	Met	Thr	His	Lys	Ile	Asp	Ala	Lys	Met	Thr	Arg	Glu	Asp
			100					105					110		

Phe	Glu	Lys	Glu	Ile	Asn	Ser	Met	Leu	Pro	Ser	Arg	Asn	Leu	Phe	Tyr
		115					120					125			

Ala	Ile	Arg	Ile	Asp	Gly	Leu	Phe	Lys	Lys	Val	Gln	Thr	Arg	Thr	Val
						135					140				

Glu	Leu	Gln	Glu	Lys	Pro	Tyr	Val	Pro	Met	Val	Glu	Ala	Val	Lys	Thr
145					150					155					160

Gln	Pro	Ile	Phe	Asn	Phe	Asp	Asn	Val	Arg	Gly	Thr	Ile	Val	Gly	Phe
				165					170					175	

Leu	Thr	Pro	Ala	Tyr	Ala	Asn	Gly	Ile	Ala	Val	Ser	Gly	Tyr	His	Leu
			180					185					190		

His	Phe	Ile	Asp	Glu	Gly	Arg	Asn	Ser	Gly	Gly	His	Val	Phe	Asp	Tyr
		195					200					205			

Val	Leu	Glu	Asp	Cys	Thr	Val	Thr	Ile	Ser	Gln	Lys	Met	Asn	Met	Asn
	210					215					220				

Leu	Arg	Leu	Pro	Asn	Thr	Ala	Asp	Phe	Phe	Asn	Ala	Asn	Leu	Asp	Asn
225					230					235					240

Pro	Asp	Phe	Ala	Lys	Asp	Ile	Glu	Thr	Thr	Glu	Gly	Ser	Pro	Glu	
				245					250					255	

<210> 70

<211> 1254

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1251)

<400> 70

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Met Thr Phe Ser Leu Phe Gly Asp Lys Phe Thr Arg His Ser Gly Ile	
1 5 10 15	
acg ctg ttg atg gaa gat ctg aac gac ggt tta cgc acg cct ggc gcg	96
Thr Leu Leu Met Glu Asp Leu Asn Asp Gly Leu Arg Thr Pro Gly Ala	
20 25 30	
att atg ctc ggc ggc ggt aat ccg gcg cag atc ccg gaa atg cag gac	144
Ile Met Leu Gly Gly Gly Asn Pro Ala Gln Ile Pro Glu Met Gln Asp	
35 40 45	
tac ttc cag acg cta ctg acc gac atg ctg gaa agt ggc aaa gcg act	192
Tyr Phe Gln Thr Leu Leu Thr Asp Met Leu Glu Ser Gly Lys Ala Thr	
50 55 60	
gat gca ctg tgt aac tac gac ggt cca cag ggg aaa acg gag cta ctc	240
Asp Ala Leu Cys Asn Tyr Asp Gly Pro Gln Gly Lys Thr Glu Leu Leu	
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aca ctg ctt gcc gga atg ctg cgc gag aag ttg ggt tgg gat atc gaa	288
Thr Leu Leu Ala Gly Met Leu Arg Glu Lys Leu Gly Trp Asp Ile Glu	
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cca cag aat att gca cta aca aac ggc agc cag agc gcg ttt ttc tac	336
Pro Gln Asn Ile Ala Leu Thr Asn Gly Ser Gln Ser Ala Phe Phe Tyr	
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tta ttt aac ctg ttt gcc gga cgc cgt gcc gat ggt cgg gtc aaa aaa	384
Leu Phe Asn Leu Phe Ala Gly Arg Arg Ala Asp Gly Arg Val Lys Lys	
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Val Leu Phe Pro Leu Ala Pro Glu Tyr Ile Gly Tyr Ala Asp Ala Gly	
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Leu Glu Glu Asp Leu Phe Val Ser Ala Arg Pro Asn Ile Glu Leu Leu	
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ccg gaa ggc cag ttt aaa tac cac gtc gat ttt gag cat ctg cat att	528
Pro Glu Gly Gln Phe Lys Tyr His Val Asp Phe Glu His Leu His Ile	
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ggc gaa gaa acc ggg atg att tgc gtc tcc cgg ccg acg aat cca aca	576
Gly Glu Glu Thr Gly Met Ile Cys Val Ser Arg Pro Thr Asn Pro Thr	
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ggc aat gtg att act gac gaa gag ttg ctg aag ctt gac gcg ctg ggc	624
Gly Asn Val Ile Thr Asp Glu Glu Leu Leu Lys Leu Asp Ala Leu Gly	
195 200 205	
aat caa cac ggc att ccg ctg gtg att gat aac gct tat ggc gtc ccg	672
Asn Gln His Gly Ile Pro Leu Val Ile Asp Asn Ala Tyr Gly Val Pro	
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Phe Pro Gly Ile Ile Phe Ser Glu Ala Arg Pro Leu Trp Asn Pro Asn	

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	245	250	255	
tgc ggc att atc atc gcc aat gaa aaa atc atc acc gcc atc acc aat				816
Cys Gly Ile Ile Ile Ala Asn Glu Lys Ile Ile Thr Ala Ile Thr Asn				
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Met Asn Gly Ile Ile Ser Leu Ala Pro Gly Gly Ile Gly Pro Ala Met				
	275	280	285	
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Met Cys Glu Met Ile Lys Arg Asn Asp Leu Leu Arg Leu Ser Glu Thr				
	290	295	300	
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Val Ile Lys Pro Phe Tyr Tyr Gln Arg Val Gln Glu Thr Ile Ala Ile				
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att cgc cgc tat tta ccg gaa aat cgc tgc ctg att cat aaa ccg gaa				1008
Ile Arg Arg Tyr Leu Pro Glu Asn Arg Cys Leu Ile His Lys Pro Glu				
	325	330	335	
gga gcc att ttc ctc tgg cta tgg ttt aag gat ttg ccc att acg acc				1056
Gly Ala Ile Phe Leu Trp Leu Trp Phe Lys Asp Leu Pro Ile Thr Thr				
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Lys Gln Leu Tyr Gln Arg Leu Lys Ala Arg Gly Val Leu Met Val Pro				
	355	360	365	
ggg cac aac ttc ttc cca ggg ctg gat aaa ccg tgg ccg cat acg cat				1152
Gly His Asn Phe Phe Pro Gly Leu Asp Lys Pro Trp Pro His Thr His				
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caa tgt atg cgc atg aac tac gta cca gag ccg gag aaa att gag gcg				1200
Gln Cys Met Arg Met Asn Tyr Val Pro Glu Pro Glu Lys Ile Glu Ala				
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His				

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<211> 417

<212> PRT

<213> Escherichia coli

<400> 71

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Thr	Leu	Leu	Ala	Gly	Met	Leu	Arg	Glu	Lys	Leu	Gly	Trp	Asp	Ile	Glu	85	90	95
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Pro	Glu	Gly	Gln	Phe	Lys	Tyr	His	Val	Asp	Phe	Glu	His	Leu	His	Ile	165	170	175
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Asn	Gln	His	Gly	Ile	Pro	Leu	Val	Ile	Asp	Asn	Ala	Tyr	Gly	Val	Pro	210	215	220
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Met	Cys	Glu	Met	Ile	Lys	Arg	Asn	Asp	Leu	Leu	Arg	Leu	Ser	Glu	Thr	290	295	300
Val	Ile	Lys	Pro	Phe	Tyr	Tyr	Gln	Arg	Val	Gln	Glu	Thr	Ile	Ala	Ile	305	310	315
Ile	Arg	Arg	Tyr	Leu	Pro	Glu	Asn	Arg	Cys	Leu	Ile	His	Lys	Pro	Glu	325	330	335
Gly	Ala	Ile	Phe	Leu	Trp	Leu	Trp	Phe	Lys	Asp	Leu	Pro	Ile	Thr	Thr	340	345	350

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Gly His Asn Phe Phe Pro Gly Leu Asp Lys Pro Trp Pro His Thr His
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His

<210> 72

<211> 8803

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
 pAN294 plasmid

<400> 72

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
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<400> 73

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
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<211> 4450

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant
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His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp	
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atc	gaa	cac	gat	gct	gtg	aaa	gtg	gaa	ttt	gca	gag	cgt	gag	cag	aaa	960
Ile	Glu	His	Asp	Ala	Val	Lys	Val	Glu	Phe	Ala	Glu	Arg	Glu	Gln	Lys	
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gca	gat	tgg	aaa	tca	gac	aga	gag	cac	cct	ctt	gaa	atc	gtt	aaa	gag	1056
Ala	Asp	Trp	Lys	Ser	Asp	Arg	Ala	His	Pro	Leu	Glu	Ile	Val	Lys	Glu	
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ttg	cgt	aat	gca	gtc	gat	gat	cat	gtt	aca	gta	act	tgc	gat	atc	ggc	1104
Leu	Arg	Asn	Ala	Val	Asp	Asp	His	Val	Thr	Val	Thr	Cys	Asp	Ile	Gly	
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tgc	cac	tcc	att	tgg	atg	tca	cgt	tat	ttc	cgc	agc	tac	gag	cag	tta	1152
Ser	His	Ser	Ile	Trp	Met	Ser	Arg	Tyr	Phe	Arg	Ser	Tyr	Glu	Pro	Leu	
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aca	tta	atg	atc	agt	aac	ggc	atg	caa	aca	ctc	ggc	gtt	gag	ctt	cct	1200
Thr	Leu	Met	Ile	Ser	Asn	Gly	Met	Gln	Thr	Leu	Gly	Val	Ala	Leu	Pro	
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Trp	Ala	Ile	Gly	Ala	Ser	Leu	Val	Lys	Pro	Gly	Glu	Lys	Val	Val	Ser	
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gtc	tct	ggc	gac	ggc	ggc	ttc	tta	ttc	tca	gca	atg	gaa	tta	gag	aca	1296
Val	Ser	Gly	Asp	Gly	Gly	Phe	Leu	Phe	Ser	Ala	Met	Glu	Leu	Glu	Thr	
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gca	gtt	cga	cta	aaa	gca	cca	att	gta	cac	att	gta	tgg	aac	gac	agc	1344
Ala	Val	Arg	Leu	Lys	Ala	Pro	Ile	Val	His	Ile	Val	Trp	Asn	Asp	Ser	
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aca	tat	gac	atg	gtg	cat	ttc	cag	caa	ttg	aaa	aaa	tat	aac	cgt	aca	1392
Thr	Tyr	Asp	Met	Val	His	Phe	Gln	Gln	Leu	Lys	Lys	Tyr	Asn	Arg	Thr	
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tct	ggc	gtc	gat	ttc	gga	aat	atc	gat	atc	gtg	aaa	tat	ggc	gaa	agc	1440
Ser	Ala	Val	Asp	Phe	Gly	Asn	Ile	Asp	Ile	Val	Lys	Tyr	Ala	Glu	Ser	

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Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp				
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gtt ctg cgt caa ggc atg aac gct gaa ggt cct gtc atc atc gat gtc				1536
Val Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val				
	500	505	510	
ccg gtt gac tac agt gat aac att aat tta gca agt gac aag ctt ccg				1584
Pro Val Asp Tyr Ser Asp Asn Ile Asn Leu Ala Ser Asp Lys Leu Pro				
	515	520	525	
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Lys Glu Phe Gly Glu Leu Met Lys Thr Lys Ala Leu				
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Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly				
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Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly				
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Leu Leu Thr Ala Asn Thr Glu Gly Asp Pro Val Val Ala Leu Ala Gly				
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Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp				
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Asn Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Glu Val Gln				
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Asp Val Lys Asn Ile Pro Glu Ala Val Thr Asn Ala Phe Arg Ile Ala				
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Ser Ala Gly Gln Ala Gly Ala Ala Phe Val Ser Phe Pro Gln Asp Val				
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Val Asn Glu Val Thr Asn Thr Lys Asn Val Arg Ala Val Ala Ala Pro				
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Lys Leu Gly Pro Ala Ala Asp Asp Ala Ile Ser Ala Ala Ile Ala Lys				
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Ile Gln Thr Ala Lys Leu Pro Val Val Leu Val Gly Met Lys Gly Gly				
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225 230 235 240

Gly Asp Leu Leu Leu Glu Gln Ala Asp Val Val Leu Thr Ile Gly Tyr
245 250 255

Asp Pro Ile Glu Tyr Asp Pro Lys Phe Trp Asn Ile Asn Gly Asp Arg
260 265 270

Thr Ile Ile His Leu Asp Glu Ile Ile Ala Asp Ile Asp His Ala Tyr
275 280 285

Gln Pro Asp Leu Glu Leu Ile Gly Asp Ile Pro Ser Thr Ile Asn His
290 295 300

Ile Glu His Asp Ala Val Lys Val Glu Phe Ala Glu Arg Glu Gln Lys
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Ile Leu Ser Asp Leu Lys Gln Tyr Met His Glu Gly Glu Gln Val Pro
325 330 335

Ala Asp Trp Lys Ser Asp Arg Ala His Pro Leu Glu Ile Val Lys Glu
340 345 350

Leu Arg Asn Ala Val Asp Asp His Val Thr Val Thr Cys Asp Ile Gly
355 360 365

Ser His Ser Ile Trp Met Ser Arg Tyr Phe Arg Ser Tyr Glu Pro Leu
370 375 380

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385 390 395 400

Trp Ala Ile Gly Ala Ser Leu Val Lys Pro Gly Glu Lys Val Val Ser
405 410 415

Val Ser Gly Asp Gly Gly Phe Leu Phe Ser Ala Met Glu Leu Glu Thr
420 425 430

Ala Val Arg Leu Lys Ala Pro Ile Val His Ile Val Trp Asn Asp Ser
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Thr Tyr Asp Met Val His Phe Gln Gln Leu Lys Lys Tyr Asn Arg Thr
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465 470 475 480

Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp
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Val Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val
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515

520

525

Lys Glu Phe Gly Glu Leu Met Lys Thr Lys Ala Leu
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<211> 23

<212> DNA

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binding site

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<223> All occurrences of n indicate any nucleotide

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23

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PanC
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: PanC
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<223> Description of Artificial Sequence: PanC
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<400> 91

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pAN336 plasmid

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<111> 1NA

<111> Artificial Sequence

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<111> Description of Artificial Sequence: Polypeptide

pAN204 plasmid

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